

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number

TO: Jeanine Goldberg

Art Unit: 1634

Location: REM-2D15&2C70 Serial Number: 10/699941

Friday, March 10, 2006

From: Beverly Shears

**Location: Biotech-Chem Library** 

**REM 1A54** 

Phone: 571-272-2528

beverly.shears@uspto.gov

#### Search Notes

Your queries have completed processing. You may access an electronic version via eDAN (SCORE) and /or http://es/ScoreAccessWeb.

**Protein Sequence Searches - February 2005** 

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

#### **Published Applications Database - November 2005**

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions .rnpbm (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published Applications AA Main) and .rapbn (Published Applications\_AA\_New).



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## STJE-Biotech/ChemLib

From:

Sent:

Goldberg, Jeanine Thursday, February 23, 2006 12:54 PM STIC-Biotech/ChemLib

To: Subject:

10/699941- ataxia-

Hello-Please search SEQ ID NO: 3.

**THANKS** Jeanine

Jeanine Anne Goldberg 1634 571-272-0743 REM 2D15 Mailbox: 2C70

3-2918NA

Searcher: Searcher Phone: Date Searcher Picked up: Date completed: Searcher Prep Time: Online Time:

Type of Search AA#: S/L:\_\_\_\_Oligomer: Encode/Transl:\_\_\_\_Tostructure #:\_\_\_\_\_To Text: Inventor: Litigation: Vendors and cost where applicable STN:\_\_\_ DIALOG: QUESTEL/ORBIT: LEXIS/NEXIS:\_\_\_ SEQUENCE SYSTEM: WWW/Internet: Other (Specify):

Date completed:	Search Site	Vendors
Searcher: Beverly e 252	STIC	IG
Terminal time: ·	CM-1	STN
Elapsed time:	Pre-S	Dialog
CPU time:	Type of Search	APS
Total time:	N.A. Sequence	Geninfo
Number of Searches:	A.A. Sequence	SDC
Number of Databases:	Structure	DARC/Questel
	Bibliographic	Other CGN

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Goldberg, J. 1016999411

GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

5, 2006, 03:15:24; Search time 14445 Seconds (without alignments) 11482.810 Million cell updates/sec March Run on:

1 gecgageetetgecageet......teteaaaaaaaaaaaa 2918 US-10-699-941-3 2918 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

5883141 segs, 28421725653 residues Searched:

11766282 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database

gb ba: \*
gb ln: \*
gb om: \*
gb ov: \*
gb pat: \*
gb pr: \* gb\_sy:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

. Description	BC026217 Homo sapi	BD171164 Novel gen		Homo		BD158743 Primer fo						CQ842483 Sequence		Homo	AC011488 Homo sapi	AC034201 Homo sapi	AX747461 Sequence	AK092298 Homo sapi
ID	BC026217	BD171164	BD183464	AB058775	AR560886	BD158743	AX881045	AK027889	AX747472	AK092309	AB052149	CQ842483	AK125457	BC008736	AC011488	AC034201	AX747461	AK092298
DB	6	9	9	80	9	9	9	80	φ	œ	80		8	80	80	14	9	œ
Query Match Length DB	2918	4976	4976	4976	3076	2894	2894	2894	2759	2759	2787	2786	2786	2276	134308	210617	2625	2625
Query Match	100.0	99.3	. 99.3	99.3	99.0	98.4	98.4	98.4	89.0	89.0	84.4	80.8	80.8	62.2	49.3	49.3	45.4	45.4
Score	2918	2896.6	2896.6	2896.6	2887.6	2870.2	2870.2	2870.2	2598.2	2598.2	2463	2357.6	2357.6	1815.8	1438.2	1438.2	1325.8	1325.8
Result No.	н		m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18

2 (bases 1 to 2918)
Strausberg, R.
Strausberg, R.
Submission (02-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer

AY220297 Homo sapi			_	_	BD150580 Primer fo			_			BC094224 Mus muscu	_		_	_	AK172939 Mus muscu			AX336690 Sequence	BD083730 Nucleic a		. AY439213 Homo sapi		BD118568 EST and e	AR423015 Sequence	
AY220297	AR560887	CQ721138	AY349150	BC048903	BD150580	AX870518	CQ832574	AB046623	BD155501	AX875439	BC094224	BC095978	BC091368	AB002365	AB050197	AK172939	AX330135	AX336310	AX336690	BD083730	BD097377	AY439213	AY423003	BD118568	AR423015	AX983709
8	9	9	0	σ	9	9	9	œ	9	9	Ó	0	σ	œ	œ	σ	9	9	9	9	9	æ	Ŋ	9	9	9
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38.2	38.1	31.6	29.4	29.4	25.5	25.5	19.8	17.9	16.1	16.1	11.9	11.7	11.4	11.3	11.2	11.2	10.9	10.9	10.9	10.8	10.8	10.7	10.7	10.6		10.6
1114.4	1113	923.2	857.8	857.8	745.2	745.2	579	522.2	470	470	346.4	341	332	330.4	327.6	326.6	318.2	318.2	318.2	315:8	315.8	311.4	311	309.8	309.8	309.8
19	20	21	22	23	24	25	26	27		c 29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1

BC026217	
LOCUS	BC026217 29-JUN-2004
DEFINITION	Homo sapiens ataxia, cerebellar, Cayman type (caytaxin), mRNA (CDNA
	clone MGC:21400 IMAGE:4153341), complete cds.
ACCESSION	BC026217
VERSION	BC026217.1 GI:20070729
KEYWORDS	MGC.
SOURCE .	Homo sapiens (human)
ORGANISM	Homo sapiens
	Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Hominidae; Homo.
REFERENCE	1 (bases 1 to 2918)
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
	Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
	Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.
	Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.
	Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.
	Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.
	Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki.S.
	Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
	Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
	McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
•	Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
	Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
-	Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
	Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
	Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
	Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M
	Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
	Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length
	human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	12477932
REFERENCE	2 (bases 1 to 2918)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (02-APR-2002) National Institutes of Health, Mammalian
	Control Collection (MCC) Course Control Collection Collection

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ARPQPEFVLPRESEERPEVAPVENRSALVSEDGETSMS"
                        WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapba-r@mail.nih.gov
Email: cgapba-r@mail.nih.gov
Contact: MGC help desk
Email: cgapba-r@mail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Bickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
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                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 20 Row: b Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
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                                                                                                                                                                                                         GACATCGAGACCCCCGATGAGACCGACTCGCTGGAGTTCCTGGGGAATGGCAACGAACTG 720
                                                                                                   GTAAGGAGGAGAGGCTGTCTCAGCTGCAGAGGGGTCATCCTGCTTCAAGCCAGTGCCTC
                                                                                                                                                                                                                                                                                                                     961 IGCTICCTICCAGACAGCAGCCTCCCCGACTACCACTACATCATGGAGAACCTCTTCCTG
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                                                                                                                                                                              TTCCCAGCTCCCATGGGGACCACCGAAGCCACGCTCCGGATGGAAAACGTGGACGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                CTTGGCAGCCCGGTGGAAGACACATCCTCTCCTCCCAACACGCTAAATTTCAACGGAGCG
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                                                                       GTAAGGAGGAGGCTGTCTCAGCTGCAGAGGGGTCATCCCTGCTTCAAGCCAGTGCCTC
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CACGCCCGGG CACGCCCCGGG ACCGGAGGTTG ACCGGAGGTTG ACCGGAGGTTG ACCGGAGGTTG ACCGGAGGTTG ACCGGAGGTTG ACCGGAGGTTG ACCGGAGGTTG ACCGGAGGTTTG ACCGGAGGTTG ACCGGAGGCTG ACCGGAGGCATG ACCGGAGGAGCATG ACCGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	
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GCCGAGCCTCTCCCAGCCCTCAGCTCCCAGAAAACACTCCCCGCAGCACCCCCCCC	QY         841 GTGATCATCGGGGGGCAAGAGCACCGTATAGACCTGCACATGCACATGAAA 900           Db         845 [

PF 26-FEB-2002 JP 2002049009 PI OSAMU OHARA,TAKAHIRO NAGASE,DAISUKE NAKAJIMA PC C12N15/09,C07K14/47//A61K31/711,A61K38/00,A61K48/00,A61P25/00,		FT CDS (404). (1489).  FEATURES Location/Qualifiers  source /organism="Homo sapiens"	/mol_type="genomic DNA" /db_xref="taxon:9606"	Query Match 99.3%; Score 2896.6; DB 6; Length 4976; Best Local Similarity 99.8%; Pred. No. 0; Matches 2911; Conservative 0; Mismatches 4; Indels 2; Gaps 1;	Qy         1 GCCGAGCCTCTGCCAGCCCTGAGCTGGAAAGCAGCTACCTCGGAGGCAGGC	Oy         61 GGCGGCGGCGATGAGAGGGGCGCAGCCGCGCGCGCTGGGGAGCCCACCGCTAAC         120           b	Qy         121 CCTGCACCCCACCCCTGCACAAAAGAGCTGGCGGCGCTGGCCACGTCGCCCTGGC         180           Db         125 CCTGCACCCCACCCCTGCACAAAGAGCTGGCGGGGGGCGCTGGCCACGTCGCCCTGGG         184	Oy 181 TGACCTTCCTCGAFGCAGAATCCGCCCTGCGAGCATCCTTCCTCCTAGGCTCTGAA 240  Db 185 TGACCTTCCTCGGATGCAGAATCCGCCCTGCGAGCATCCTTCCT	Oy         241 GGCCGGGGAGCGTGAGCGTGCCCAGCTGCACCCGGGCAGGGCTCGCCTTTGTTTG	Qy         301 GTAAGGAGGAGGCTGTCTCAGCTGCAGAGGGTCATCCTGCTTCAAGCCAGTGCCTC 360           Db         305 GTAAGGAGGAGAGGCTGTCTCAGCTGCAGAGGGGTCATCCTGCTTCAAGCCAGTGCCTC 364	Qy         361         TTCCCAGCTCCCATGGGGACCACGCCACGCTCCGGATGGAAAACGTGGACGTGAAG         420           bb         165         TTCCCAGCTCCCATGGGGACCACCGAAGCCACGCTCCGGATGGAAAAACGTGGACGTGAAG         424	Qy         421 GAGGAATGGCAGGAGGACTTCCCAGGCCACTCCCAGAAGAGACGCGGGGTGCAACTG         480	OY 481 CTTGGCAGCCCGGTGGAAGACACATCCTCTCCTCCAACACGCTAAATTTCAACGGAGCG 540	Qy         541 CATCGTAAGAGGAAGACGCTGGTGGCCCCAGAGATCACATTTCTCTGGATCAGAGTGAG         600	Qy 601 GGGTCCCTGCTGTGCCGATGACTTCTTGGATACCCTGATGACCTGGATATTAACGTGGAT 660	661	Db 665 GACATCGAGACCCCCGATGAGACTGGCTGGAGTTCCTGGGGAATGGCAACGACTG 724  Oy 721 GAGTGGGAAGACGACCCCCGTGGCCACCGCCAAGAACATGCCCGGGGACAGCGCGGAT 780	Db 725 GAGTGGGAACACCCCCGTGGCCACCGCCAAGAACATGCCCGGGGAACAGCCGCGAAT	Oy 781 CTATTTGGGGACGGCACGACGGACGCCCCCCCACGGGCCCCTGTGGCGGACA 840
2161 ATTGCAAAATGACACCCCAGTAATCTAGAACATTCTCAAGCCCCTTTAACTCAGATGTCA 2220 2163 ATTGCAAAATGACACCCCAGTAATCTAGAACATTCTCAAGCCCCTTTAACTCAGATGTCA 2222	2221 AGCCACCGGGCAAACCCGGTCAATACCTCCCACGAAGGAATGAGATATGTGGACCTCACT 2280		2341 AGGCTCAGAAACTGGCTCTGAAATAGGCAGACCTAGCAAGAGGAAGATACAGGGTATCGG 2400 	2401 GCGTTTGAGTGTTTCAGAAGTCATTCGGGAAGATAAATCCAGTGCGCTGGCCGCAGCCAC 2460 	2461 CTGCATTCAAAGCTTGGACCGGGTTCTTGTTCGGGAGGCAAATTTCCCTAGGAAAAA 2520 		2581 CACTGAGCTCCCTGTCTCTGGAAGTATTTAAGAAAAGGCTGGGCCAGGCACGATGGCTCA 2640 	2641 CGCCTGTAATCCCAGACTTTGGGAGGCCGAGGCAGGCGGATCACCTGAGGTGAGGTTT 2700 	2701 GAGAACAGCCTGGCCAACATGGTGAAACCTCATCTGTAAAAATACAAAAATTAGCCA 2760 	2761 GGCGTGGTGGCGGGGCGTGTAATCCCAGCTACTTGGGAGGCTGAGGATGAGAATCACT 2820 	71-66 71-66 71-66		SULT 3 183464	CUS BD183464 4976 bp DNA linear PAT 17-JUN-2003 FINITION Novel genes and proteins encoded by the genes. CESSION BD183464 1 CT.2107664	YWORDS JP 2002345492-A/177. URCE Homo sapiens (human)			JOORNAL FACENT: UP 2002,545492-A 177 03-DEC-2002; KAZUSA DNA RESERARCH INSTITUTE OS Homo sapiens (human)	PN JP 2002345492-A/177 PD 03-DEC-2002

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1025 TACGTCATCAGCAGCTTAGAGCTCCTGGTGGCTGAGGACTACATGATCGTGTACCTGAAC 1084
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                                                                                                                                                                                  425 GAGGAATGGCAGGACGAGGTCTTCCCAGGCCACTCCCAGAAGAGACGGGGGTGGAACTG
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                                                                                                                                                                                                                                                                                                                                                                          605 GGGTCCCTGCTCCGATGACTTCTTGGATACCCCTGATGACCTGGATATTAACGTGGAT
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DNA Res. 8 (2), 85-95 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tränslation="PSSDAESAPASILFILGSEGPGSVSDAQIHPGRARLCLPVRRGG
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IRTPDETDSILEFLGNGNBLEWEDDTPVATAKNNFGDSAADLFGDGTTEDGSAANGRLMR
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LEVYVISSLEBLLVABDYMIVYLMGAPPRRAMPGIGMLKKCYQHIDRELKKNILKSLIIV
HPSWFIRTVLAISEPFISVYEINKTQYVHSLEDLEQLIPMEHVQIPDCVLQYEBERLK
ARRESARPQPEFVLPRSEBKKPEVAPVGRRSALVSEDQETSMS
                                                                                                                                                                                                                                                                                                 Submitted (27-MAR-2001) Osamu Ohara, Kazusa DNA Rsearch Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (R-mail:cdnainfo@kazusa.or.jp, ULL.http://www.kzausa.or.jp/huge, Tel:81-438-52-3913,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCGGGCGGCGATGAGGGGGGGCGCAGCCCCCCCCGCGTGGGGAGCCCCACCGCTAAC 120
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                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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   for KIAA1872 protein, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                          1. .4976
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hi05518"
/tissue_type="brain"
/note="vector:pBluescriptil SK plus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Start codon is not identified.

Codon start=1

/product="KTAA1872 protein"

/db_xref="GI:14017961"
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                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/gene="KIAA1872"
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/gene="KIAA1872"
   Homo sapiens mRNA for K.
AB058775
AB058775.1 GI:14017960
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                                                                sapiens (human)
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Matches 2911; Conservative
                                                                                                                            Hominidae; Homo.
                                                                                Homo sapiens
                                                                                                                                              (sites)
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/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"  ORIGIN Query Match Best Local Similarity 99.7%; Pred. No. 0; Matches 2886; Conservative 0; Mismatches 8; Indels 1; Gaps 1; Ov 8 CTCTGCCAGCCCTGAGCTGGGAAGAAGCAGCTACCTGAAGCAGGGGGGGG		666TGACCTT             666TGACCTT 3AAGGCCCGG			Qy         488 GCCCGGTGGAAGACACATCTTCTCCTCCCAACACGTAATTTCAACGGAGCGCATCGTA 547           Db         481 GCCCGGTGGAAGACACATCTTCTCTCCTCCCTAATTTCAACGGAGCGCATCGTA 540           Qy         548 AGAGGAAGACGCTGGTGGCCCCAGAGATCATCTCTGGATCAGATCAGGGGTCCC 607           Db         541 AGAGGAAGACGCTGGTGGCCCCAGAGATCAACATTTCTCTGGATCAGGTGAGGGGTCCC 607	QY         608 TGCTGTCCGATGACTTCTTGGATACCCTGATGACCTGGATATTAACGTGGATGACATCG 667           Db         601 TGCTGTCCGATGACTTCTTGGATACCCCTGATGACCTGGATATTAACGTGGATGACATCG 660           QY         668 AGACCCCGGATGAGACCGACTGGAGGATCCTGGGGAATGGCAACGAACTGGAGTGGG 727           Db         661 AGACCCCCGATGAGACCGACTGGTGGAGTTCCTGGGGGAATGGCAACGAACTGGAGTGGG 720	Qy         728 AAGACGACCCCCGTGGCCACGCCAAGAACATGCCCGGGGACAGCGCGGATCTATTTG         781	QY         848 TCGGGGAGCAAGAGCACGTATAGACCTGCACATGATCCGGCCTTACATGAAAGTGGTCA 907           Db         841 TCGGGAGC-AGAGCACCGTATAGACCTGCACAGATGCGCCTTACATGAAAGTGGTCA 899           QY         908 CCCACGAAGGGTACTACGCGAAGGCCTCAACGCCATCATCGTCTTCGCAGCTGCTCC 967           Db         900 CCCACGGAGGTACTACGGCGAAGGCCTCAACGCCATCATCGTCTTCGCAGCCTGCTTCC           Db         900 CCCACGGAGGGTACTACGGCGAAGGCCTCAACGCCATCATCGTCTTCGCAGCCTGCTTCC
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	GGGCAAACCCCGTCAATACCTCCCACCAAGGAATGAGATTGTGGAACCTCCCCCCCC			2648 AAICCCAGACTITIGGGAGGCCGAGGCGGATCACCTGAGGTGAGG	2768 TGGCAGGTGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGATCACTTAAACCT 2827  [	2888 GCAAGACTCTGTCTC 2902 	AX881045  Sequence 15950 from Patent BP1074617.  NAX881045  AX881045.1 GI:40035781  Homo sapiens (human)  SM Homo sapiens (human)  Homo sapiens (human)  Nammalia; Butheria; Craniata; Vertebrata; Euteleostomi;  Hominidae; Homo.
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	1148 GGAGGTTGCGGAAAACCTGAAGTCCTTGATCATCGTCGTCGTTGTTGTGA 1207	1260   TGCACAGCTTGGAAGCTGGAGCTATCGCTTATGGAACACGTCCAGATCCCAGACT   1319     1328   GCGTCCTGCAATACGAAGGAAAGACTGAAGCCAGGAGGAGGAGGCCCCAGC   1387	CTGCTCTGGTCTCAGAAGATCAGAAACAAGCATGTCCTGAGGGGACGTGAGCATAACAA	ATCTCATCCTGCCTCATCCTGAGTCCCGAAGGGTGCCAGCCCCCCCGCAAGGGTGCCAGCCCCCCCC	ACACTCA ACACTCA ACACTCA SGTGGCC	1808 TCCGCTCCTGCTCGCAGCCCCTGTGGTCAGAGCTGGATACAAGATTCAAGACCCTTCTCT 1867 	1868 TGCTTGTCACCCGCTCCAGGTTGAGCCACAGACCCACCCCCCCC

128   AAGACGACCCCCGTGGCCAAGAACATGCCCGGGGACAGCGCGGATCTATTG   187	TCAGCAGCTTAGAGCTCCTGGTGGCTGAGGACTACATGATCGTGTACCTGAACGGTGCCA	1148   GGAGGTTGCGGAAAAACCTGAAGTCCTTGATCATCGTCCACCCCTGGTGGTTCGGA 1207	TGCACAGCTTGGAAGACCTGGAACTCATCCCTATGGAACAGGTCCCAGACT	1388   CGGAGTTTGTGCTGCCAGGTCTGAAGAGAGCCAGAGGTGGCACCAGTGGAAAACAGGT		ATCTCALICION	1688 GCAGTATTTGTGCGTTCCAGAAAGGGCCCAGCTCTGAGCCCCTTCCACACTCA 1747  1680 GCAGTATTTGTGCGTTCCAGAAAAGGCCCCAGCCTTCGAGCCCCTTCCACACTCA 1749  1680 GCAGTATTTGTGCGTTCCAGAAAAAGGCCCAGGCTCTGGAGCCCCTTCCACACTCA 1739  1748 GCAGTTCTCAGCCGAGGAGGCCAGGGGGGGGGGGGGCCCGCGTGGCCTTCAGCGTGGCCTTCAGCGGTGGCCTTCAGCGGGGGGGG
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AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsui,A., Nagai,K. and Otsuki,T. TITLE Primers for synthesising full-length cDNA and their use JOURNAL Patent: EP 1074617-A 15950 07-FEB-2001; Research Association for Biotechnology (JP) Research Association for Biotechnology	IGIN  Query Match Best Local Similari Matches 2886; Cons	68 68 61 128	121 CCCACCCACCCTGCAAAAAGAGCTGGCGGGGGCTGGCCACGTCGCCTGGGGTGACCTT  188 CCTCGGATGCAGAATCCGCCCTGCGAGCATCCTCTTCCTCCTAGGCTCTGAAGGCCCGG		GGAAT TGGCA TGGCA TGGCA		Qy         608         TGCTGTCCGATGACTTCTTGGATACCCCTGATGACTGAGATATTAACGTGGATGACATCG         667           Db         601         TGCTGTCCGATGACTTCTTGGATACCCCTGATGACCTGGATATTAACGTGGATGACTCG         660           Qy         668         AGACCCCCGATGAGACTCGCTGGAGTTCCTGGGGAATGGCAACGAACTGGAGTGGG         727           Db         661         AGACCCCCGATGAGACTCGCTGGAGTTCCTGGGGAATGGCAACGAACTGGAGTGGG         720           Db         661         AGACCCCCGATGAGACTCGCTGGAGTTCCTGGGGAATGGCAACGAACTGGAGTGGG         720

	Db   841 TCGGGGAGC-AGAGCACCGTATAGACCTGCACATGATCGAGCTTACATGAAGTGGTCA 899	960 TICCAGACAGCAGCCTCCCCGACTACACATCATGGAGAACCTCTTCCTGTACGTCA	Qy 1028 TCAGCAGCTTAGAGCTCCTGGTGGCTGAGACTACATGATCGTGTACCTGAACGGTGCCA 1087	AN 1088 CGCCCGGCGGAGGATGCCTGGAATCGGCTGAAGAAGTGCTACCAGATGATCGACC 1147	Oy 1148 GGAGGTTGCGGAAAAACCTGAAGTCCTTGATCATCGTCCTCGTGGTTCATTCGGA 1207	Ay 1208 CTGTGCTGGCCATCTCTCGCGCTTTCATCAGCGTCAAGTTCATCAAGAAGTCCAGTACG 1267	Qy 1268 TGCACAGCTTGGAAGACCTGGAGCAACTCCTTTGGAACACGTCCAGACT 1327	Qy         1328         GCGTCCTGCAATACGAAGAGGAAGACTGAAGACCAGGAGGGGAGAGCCCCAGC         1380         GCGTCCTGCAATACGAAGAGAAAGACTGAAGGCCAGGAGAGAGA	Oy 1388 CGGAGTTTGTGCTGCCCAGGTCTGAAGAGCCCGAGGTGGCACCCAGTGGAAAACAGGT 1447	Oy 1448 CTGCTCTGGTCTCAGAAGATCAGGAAACATGTCCTGAGGCGACGTGAGCATAACAA 1507	Oy 1508 AGACATGGAAGATCCAGATGCCAGAAAACCTCTGTCAGACGCCCACTGGCCCAG 1567	Qy 1568 ATCTCATCCTCAGCTCCTCAATCCTTCCAAGGTGCCAGCCCCTCCGTTCATC 1627	Oy 1628 TCTGAAACCCAGCATCCTTTTCAGCTGGAAACATTGTATTTTTTTT	Oy 1688 GCAGTATTGTGCGTTCCAGAAAAGGGCCCAGCTCTGAGCCCCTCACCCTTCCACACTCA 1747	Oy 1748 CGAACTCTCAGCCGAGGAAGGCAGCAGGGGGTGGCCCGCGTGGCGTGGCC 1807	Oy 1808 TCCGCTCCTGCTCGCAGCCCTGTGGTCAGAGTGAATACAAGATTCAAGACCCTTCTCT 1867	QY         1868         IGCTTGTCACCCGCTCCAGGTTGGAGCCACAGACCCACCGCCACCGCCGGCTGGGTTG         1927           Db         1860         TGCTTGTCACCCGCTCCAGGTTGGAGCCACAGACACCCACC	Oy 1928 CGTCCTTTCCTGTGCCTTTCCCTCAGAATGCGGCCTCAGACCTAGAAGCTCAACCCCCC 1987
Loc	BOUICE 12894 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9666" /clone="Y79AA1000268" /cell_line="Y99"	/clone lib="Y79AA1" /note="cloning vector: pME18SFL3" ORIGIN	Query Match 98.4%; Score 2870.2; DB 8; Length 2894; Best Local Similarity 99.7%; Pred. No. 0; Matches 2886; Conservative 0; Mismatches 8; Indels 1; Gaps 1;	39GAAGAAGCAGCTACCTCGGAGGCAGGCGCGCGCAGGCGGC 67	()()	18	3000GG 24			AGGAAT        AGGAAT			Oy         548         AGAGGAAGACGCTGGTGGCCCCAGAGATCAACATTTCTCTGGATCAGAGTGAGGGTCCC         607           Db         541         AGAGGAAGACGCTGGTGGCCCCAGAGATCAACATTTCTCTGGATCAGAGTGAGGGGTCCC         600	CATCG	167666        	AAGACGACACCCCCTTGCCACGCCAAGAACATGCCCGGGACAGCGCGCATCTATTTG	788 GGGACGCACGACGACGCCGCCACCGCCAACGGCCCCTGTGGCGGACAGTGATCA	DD 781 GGGGGGGCGCGGCGGCGGCGCCGCCCAACGGGGCGCCCTGTGGCGGCGCTCA 840 , Qy 848 TCGGGGAGCAAGAGCACCGTATAGACCTGCACATGATCCGGCCTTACATGAAAGTGGTCA 907

KEYWORDS SOURCE SOURCE GRANISM Homo sapiens ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; REFERENCE 1 AUTHORS Isogai, T., Suqiyama, T., Otsuki, T., Wakamatsu, A. Saro H. Ishii S.	Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuho,Y. Full-length CDNA sequences Patent: EP 1308456-4 997 07-MAY-2003.	Helix Re Biotechr ce	/organism="Homo sapiens" /mol_type="mkNA" /db_xref="taxon:9606"	Query Match 89.0%; Score 2598.2; DB 6; Length 2759; Best Local Similarity 95.2%; Pred. No. 0; Matches 2756; Conservative 0; Mismatches 3; Indels 136; Gaps 2	AAGAAGCAGCTACCTCGGAAGGCAGGCGGCGCGCGCGCGC			QY         188 CCTCGGATGCAGAATCCGCCCTGCGAGCATCCTCCTTAGGCTCTGAAGGCCCGG         247           Db         129CCCCTGCGAGCATCCTCTCTCCTCTAGGCTCTGAAGGCCCGG         170	QY         248 GGAGCGTGAGCGATGCCCAGCTGCACCCGGGCAGGCTCGCCTTTGTTTG	GY         308 GGAGAGGTGTCTCAGCTGCAGAGGGTCATCCTGCTTCAAGCCAGTGCCTCTTCCCAG         367           Db         231 GGAGAGGTGTCTCAGCTGCAGAGGGGTCATCCCTGCTTCAAGCCAGTGCCTCTTCCCAG         290	Oy 368 CTCCCATGGGACCACCGCACGCTCCGGATGGAAAACGTGAAGGAGGAAT 427	OY 428 GGCAGGACGAAGATCTTCCCAGGACCAGAAGACGGGGGGGG	Oy 488 GCCCGGTGGAAGACACATCCTCTCCCCCAACAGCGCTAAATTTCAACGAAGCGCATCGTA 547	QY         548 AGAGGAGGCGCTGGTGGCCCCAGAGATCAACATTTCTCTGGATCAGAGTGAGGGCTCCC         607           Db         405 AGAGGAAGACGCTGGTGGCCCCAGAGATCAACATTTCTCTGGATCAGATGAGGGGTCCC         464	Qy 608 TIGGTGCGATGACTTCTTGGATACCCCTGATGACCTGGATATTAACGTGGATGACATCG 667	Oy 668 AGACCCCGGATGACCCGACTCGCTGGAGTTCCTGGGGAATGGCAACGAACTGGAGTGGG 727 
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1808   TCCGCTCCTGCAGCCCTGTGGTCAGAGCTGGATTCAAGACCCTTCTTT   1867	1988 TATGAGGGCCACGTCCTGGGGTAGCTCCTGACCTCCGACCTTATGTCCAATTTCACACC 2047 1845 TATGAGGGCCACGTCCTGGGGTAGCTCCTGACCTCCGACCTTATGTCCAATTTCACACC 1904 2048 CATGGTTTTTCATTTGACCGCCCCCTTCTCGGCTCATATGACACCCCTTTGAGA 2107 1905 CATGGTTTTTCATTTGACCCGCCCCCTTCTCGGCTCATAATGACACCCAGCTCCTTTGAGA 1964	2108 GGATCAGAGCCATTGCACAAGAAGAGCGCTGCCAACCATCCTTGTCCTCCGATTGCAA 2167 1965 GGATCAGAGCCCATTGCACAAGAAGAGCGCTGCCAACCATCCTTGTCCTCCGATTGCAA 2024 2168 AATGACACCCAGTAATCTAGAACATTCTCAAGCCCCTTTAACTCAGATGTCAAGCCCC 2227 2025 AATGACACCCCAGTAATCTAGAACATTCTCAAGCCCCTTTAACTCAGATGTCAAGCCAC 2227 2025 AATGACACCCCAGTAATCTAGAACATTCTCAAGCCCTTTAACTCAGATGTCAAGCCACC 2084	2228 GGGCAAACCCGTCAATACCTCCCACCAAGGAATGAGATATGTGGACCTCACTGCTCCCC 2287  [	GAPACTGGCTCTGAAATAGGCAGACCTAGCAAGAGAAGATACAGGGTATCGGGCGTTTG	2265 AGFGTTTCAGAAGTCAFTCGGGAAGATAAATCCAGTGGCGCTGGCCTCGGCCTCGCTTG 2324 2468 CAAAGCTTGGACCAGCGGGTTCTTGTTCGGGAGGCAAATTTCCCTAGGAAAAGAAGAACA 2527 2325 CAAAGCTTGGACCAGCGGGTTCTTGTTCGGGAGGCAAATTTCCCTAGGAAAAGAAGAACA 2384	2528 GACTTTTCTAATGTGGTCCAAATGCGGATCACTGGTCAGATGGACTCTAGAAGCACTGAG 2587  [	0 0 0	2565 GCCTGGCCAACATGGTGAAACCTCATCTTACTAAAAATACAAAAATTAGCCAGGGTGG 2624 2768 TGGCAGGTGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCATGAGAATCACTTAAACCT 2827 2625 TGGCAGGTGCCTGTTATCCCAGCTACTTGGGAGGCTGAGGCATGAGAATCACTTAAACCT 2827 2625 TGGCAGGTGCCTGTTATCCCAGCTACTTGGGAGGCTGAGGCATGAGAATCACTTAAACCT 2684	2828 GACAGGCACAGGTTACACTGAGCCAAGATCGTGCCACTGCATTCCAGCCTGGGCCACAGA 2887 [
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                 ir, National Institute of Technology
for full insert sequencing: HRI and
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hote="cloning vector: pME188FL3"
296. 1345
/note="unnamed protein product"
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Pred. No. 0;
0; Mismatches
                                                                                                                                                       /organism="Homo sapiens"
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/db xref="taxon:9606"
/clone="cocBBF2011137"
/tissue type="brain"
/clone_lib="OCBBF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /proteIn_id="BAC03859.1"
/db_xref="G1:21750875"
                 HRI, and Biotechnology Center,
                                         Evaluation, clone selection f
RAB; annotation: HRI and RAB.
Location/Qualifiers
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Best Local Similarity 95.2
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2759 bp mRNA linear PRI 30-JAN-200
Homo sapiens cDNA FLJ34990 fis, clone OCBBF2011137, moderately
similar to BCL2/ADENOVIRUS BIB 19-KDA PROTEIN-INTERACTING PROTEIN
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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oligo capping; fis (full insert sequence)
Homo sapiens (human)
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(bases 1 to 2759)
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...denetic Resources; 23-1, Toyan

..., 162-8640, Japan

...p, URL:http://www.nih.go.jp/yoken/geneban.
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R. Site2: DralII (CACTATO)

Rescription: lst strand cDNA was primed with an oligo(dT) primer (ATGTGGCTTTTTTTTTTTTTT) double-stranded cDNA was synthesized using specific 5 and 3' primers and amplified by PCR. The PCR product was digested with Sfit and size selection was performed to exclude fragments 41.5kb.The Sfit and size selection was performed to exclude fragments 41.5kb.The Sfit and size selection was performed to exclude fragments 41.5kb.The Sfit and size selection using selection was performed to exclude fragments 41.5kb.The Sfit and size selection using the product was digested with Sfit and size selection use cloned into distinct DralII sites of pwRalBs-Fla. XhoI sites june; used for sequencing (5 send primer [CTACTCTCTAAAGCTGCG];

... constructed by Sugano et al. (University of Tokyo, Institute of Seconstructed DralII sites can be used for sequencing (5 send primer [CTACTCTCTAAAGCTGCG];

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// clone="mank" "Resourced the coration of the cora
AB052149 2705 Macaca fascicularis brain cDNA, clone:QccE-20783, similar to human carearin (ATCAY), mRNA, NM_033064.
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/translation="MGTTEATLRMENVDVKEEWQDEDLPRPLPEETGVELLGSPVEDT
SSPPNTLARNGAHRKRKTLVAPDINISLDQSEGSLLSDDFLDTPDDLDINVDDIETPD
RTDSLRFLGNGNELEWGDDTPVATAKNMPGDSADLFGDGTTEDGGAANGRLMRTVIIG
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ISSLELLVAEDYMIVYLNGATPRRRMPGIGMLKKCYQMIDRRLRKNLKSLIIVHPSWP
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Direct Submission

Birect Submission

Submitted (Os-DEC-2000) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
I-chome, Shinjuku-ku, Tokyo, 162-8640, Japan

(B-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/,
Tel:81-35-285-1111(ex.2120), Fax:81-3-5285-1181)
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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/clone_lib="macaque brain cDNA library QccB"
/dev_stage="adult"
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Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
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'protein id="BAB19004.1"
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10.21   TAGENCY COCCOCCUS AND ACCOUNTY CONTRICTORY C	Db 2004 TCACACCGGGGTTTTTCATTTGACCGGCCCCTTCTCGCTCATAATGACACCAGGTCC 2103 Oy 2101 TTTGAGAGGATCAGAGCCCATTGCAAAAAAGAGCGGCTGCCAACCATCGTTGTCCTCG 2160	Db 2104 TTTGAGAGGATCAGAGCCCATTGCACAGAGAGCTGCCAGCTGCCATCTTGTCTCTG 2163  Qy 2161 ATTGCAAAATGACACCCCAGTAATCTAGAACATTCTCAAGCCCCTTTAACTCAGATGTCA 2220	2164	Db   2224 AGCCACAGGGCAAACCCAGTCAATACCTCCCACCAAGGAATGAGATATGTGGACCTCACT   2283   Qy   2281 GCTCCCCCAACCCAGGGTCAGGACACGCCAAGGCAGGACGCAAGGCGGATTGGAACAGCAG	QY         2341 AGGCTCAGAAACTGGAATAGGCAGACCTAGCAAGAAGAAGATACGGTATCGG         2400           Db         2344 AGGCTCAGAAGCTGCTGAAATAGACCTAGCAAAAGGAAGATACAGGTAT         2396	OY 2401 GCGTTTGAGTGTTTCAGAAGTCATTCGGGAAGATAAATCCAGTGCGCTGGCCGCAGCCAC 2460 Db 2397	OY 2461 CTGCATTCAAAGCTTGGACCAGGGGTTCTTGTTCGGGAGGCAAATTTCCCTAGGAAAAA 2520	OY 2521 GAAGACAGACTTTTCTAATGTGCTCCAAATGCGGATCACTGGTCAGATGGACTCTAGAAG 2580  Db 2439 GAAGACAGACTTTCTAATGTGGTCCAAATGCCGGTCACTGGTCAGATGGACTCTAGAAG 2498	Qy       2581 CACTGAGCTCCCTGTCTCTGGAAGTATTTAAGAAAAGGCTGGGCCAGGCACGATGGCTCA 2640         Db       2499 CAGTGAGCTCCCTGTCTCTGGAAGCATTTAAGAAAAGGCTAAGGCGGGGCACGATGACTCA 2558	Oy 2641 CGCCTGTAATCCCAG-ACTTTGGGAGGCCGAGGCAGGCGGATCACCTGAGGTGAGGGTT 2699	Oy 2700 TGAGAACAGCTGGCCAACATGGTGAAACCTCATCTACTAAAAATACAAAAATTAGCC 2759	Qy 2760 AGGCGTGGTGGCAGCTGCTAATCCCAGCTACTTGGGAGGCTGAGGCATGAGAATCAC 2819	<pre>Qy 2820 TTAAACCTGAGAGGCAGAGGTTACAGTGAGCCAAGATCGTGCCACTGCA 2868</pre>	CQ842483	DEFINITION Sequence 1130 from Patent EP1440981. ACCESSION CQ842483 VERSION CQ842483.1 GI:50894270 KEYWORDS .	×	RS RS	TITLE Full-length human cdna JOURNAL Patent: BP 1440981-A 1130 28-JUL-2004; Research Association for Biotechnology (JP)
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		1028 TACGTCATCAGCAGCTTAGAGCTCCTGGTGGGGCTGAGGACTACATGATCGTGTACCTGAAC 1081 GGTGCCACGCCGGGGGGAGATGCCTGGAATCGGCTGGCTG	1088 GGCGCCCCGGCGAAGAAGCCGGGGATCGGCTGACGAAGAAGTGCTAGAGAGTGCTAGATGCCGGGGAATCGCCTGAAGAAGTGCTAGAGAGTCGTTGAAGTCGTCGAAGTCCTCGTGGGTTGCGGGAAAAACCTGAAGTCCTTGATCATCGTCGACGCTCGTGGTTC	1148 ATCGATCGGAGATTGCGGAAAAACCTGAAGTCCTTGATCATCGTCCACCCCTCGTGGTTC 1201 ATTCGGACTGTGCTGGCCATCTCGCCCTTCATCAGCGTCAAGTTCATCAAGAAGATC	1208 ATTCGGGACTGTGCTGGCCATCTCGGCCCTTTCATCAGGGAGAGTTCATCAACAAGATC 1261 CAGTACGTGCACAGCTTGGAAGACCTGGAGCAACTCATCCCTATGGAACACGTCCAGATC 1268 CAGTACGTGCACAGCTTGGAAGAACGAACTCATCCCTATGGAAAACGTCGAGATC 1268 CAGTACGTGCACAGCTAGAAGAACCTCATCCCATGGAAAACGTCAGAATC	1321 CCAGACTGCGTCCTGCAATACGAAGAGGAAAGACTGAAGGCCAGGAGGGGAGAGGCGAGGG 1328 CCAGACTGCGTCCTGCAATACGAAGAGGAAAAGACTGAAGGCCAGGAGGAAGAGGAGAAGAGGAAAAGACTGAAGGAGAAGAGAAGAGAAAAGACTGAAGAGAAGAGAAAAGACGAAGA	1381 CCCCAGCCGGAGTTTGTGCTGCCCAGGTCTGAAGAGAAGCCAGAGGTGGCACAGTGGAA 	1441 AACAGGTCTGCTCTGGTCTCAGAAACAGGAAACAAGCATGTCCTGAGGCGACGAGGAGCGACGAGCGACGAGCGACGAGCGACGA	1501 ATAACAAGACATGGAAGAAGATTCCAGATGCCAGAAACCTCTGTCAGACGCCCACTG	1561 GCCCAAQATCTCATCCTCCTGAGTCCCAATCTTCCAAGGTGCCAGCCCTCC 1	1621 GTTCATCTCTGAAACCCGGCATCCTTTTCAGCTGCTTGAAAACATTGTATTTTTTTT	1681 TAACGATGCAGTATTTGTGCGTTCCAGAAAAGGGCCCCAGCTCTGAGCCCCTTCC	1741 ACACTCACGAACTCTCAGCCGAGGAAGGCAAGAAGCGCAGGGGGTGGCCGCGGGGGGGG	1801 GGTGGCCTCCGCTCGCAGCCCCTGTGGTCAGAGCTGGATACAAGATTCAAGACC- 	1861 CTICTCTTGTCACCCGCTCCAGGTTGGAGCCACAGACACCCCCGCCACCCCGGCT	1921 GGGTCTGCGTCCTTTCCTGTGCCTTTCCCTCCAGAATGCGGCCTCAGACGTCAGAAGCTCAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	1981 ACCCCCTATGAGGCCACGTCCTGGGGTAGGTCCTGACCTCCGACCTTATGTCCAAATT  1985 ACCCCC-AGGAGGCCACGTCCTGAGGTACCTCCTGGCCTCTGACCTTACGTCCAAAAT	2041 TCACACCCATGGTTTTCATTTGACCCGCCCCTTCTCGCTCATAATGACACCCAGCTCC

0) (1	Db 779 CAITCGGACTGGCCGTCTCTCGCCCTTTCAICAGCGTCAAGTTCATCAAGAT 838     Qy	Length 2786;   Day   1320   CCCAGACTGCGTCCTGCAAGAGGAAAGACTGAAGGCCAGGAGGAGGGGGG   1379   Day   CCCAGACTGCGTCCTGCAATACGAAGACTGAAGACTGAGGAGGGGGGG   1379   Day   CCCAGACTGCGTCCTGCAAGAGAAGACTGAAGACTGAAGACTGAAGACTGAAGACTGAAGACTGAAGACTGAAGACTGAAGACTGAAGACTGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	STGAA 419 OY 1440	ANACT 479 Qy 1500	OY         1560 GGCCCCAGATCTCATCCTGAGTCCTAATCTTCAAGGTGCCCAATCTTCAAGGGTGCCCCTC         1619	QY         1620         CGTTCATCTCTGAAACCCAGCATCTTTTCAGCTGAAAACATTGTATTTTTTTT	SAACT	GCGGA 779 CY 1800	GGAC 		Qy         2040         TTCACACCCATGGTTTTTCATTTGACCCGCCCCTTCTCGCTCATAATGACACCCAGCTC         2099	TIGAL TIGAL	CAGAT 	
A H OWA	ource	Nety Match 10 Similarity 95.2%; Pred. No. 0; 11 Conservative 0; Mismatches 4; Indels 1300 AGTAAGGAGAGAGGCTGTCTCAAGCTGCAAGGGGTCATCCCTGCTT 1 AGTAAGGAGAGAGAGGTTGTTCAAGCTAGCAAGGAGAGAGA	360 CTTCCCAGCTCCCATGGGGACCACCGAAGCCACGCTCCGGATGGAAAACGTGAAO 61 CTTCCCAGGCTCCCATGGGGACCACCGAAGCCACGCTCCGGATGGAAAACGTGAAO 61 CTTCCCAGGCTCCCATGGGGACCACCGAAGCCACGCTCCGGATGGAAAACGTGGACA	420 GGAGGAATGGCAGGACGAAGATCTTCCCAGGCCACTCCCAGAAGAGACGGGGGGTG 	480 GCTTGGCAGCCGGTGGAAGACACATCCTCTCCTCCCAACACGCTAAATTTCAACA 	540 GCATCGTAAGAGGAAGACGCTGGTGGCCCCAGAGATCAACATTTCTCTGGATCAGAGTGA 		GGAGTGGGAAGACGCCCCGTGGCCACCGC	TCTATTTGGGACGCACGACGGAGGGCGCACGCACGCACGC					

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NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Halix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CCBBF2037068"
/tissue_type="brain"
/clone_ILb="CCBBF2"
/dev_stage="fetal"
/note="cloning_vector: pME18SFL3"
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95.2%; Pred. No. 0;
ive 0; Mismatches
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Homo sapiens CDNA FLJ43468 fis, clone OCBBF2037068, moderately similar to BCL2/adenovirus B1B 19-kDa protein-interacting protein
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Unpublished
Upublished
2 (base 1 to 2786)
1809al.T. and Yamamoto, J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamateari, Kisarazu, Chiba 292-0818, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                  CCTGCATTCAAAGCTTGGACCAGCGGGTTCTTGTTCGGGAGGCAAATTTCCCTAGGAAAA
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                 GAGGCTCAGAAACTGGCTCTGAAATAGGCAGACCTAGCAAGAGGAAGATACAGGGTATCG
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AK125457.1 GI:34531558
Oligo capping; fis (full insert sequence)
Homo sapiens (human)
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1679 CTTTGAGAGGATCAGAGCCCATTGCACAAGAAGAGCCGCTGCCAACCATCCTTGTCCTCC 1738	2160 GATTGCAAAATGACACCCCAGTAATCTAGAACATTCTCAAGCCCCTTTAACTCAGATGTC 2219	2220 AAGCCACGGGCAAACCCGTCAATACCTCCCACCAAGAATGAGATATGTGGACCTCAC 2279	2280 TGCTCCCCGAACCCAGGTCAGGCTGGGACACGCCAACGCTGTTCCGGGTTGGAACAGCA 2339	-2340 GAGGCTCAGAAACTGGCTCTGAAATAGGCAGACCTAGCAAGAGGAAGATACAGGGTATCG 2399 	2400 GGCGTTTGAGTGTTTCAGAAGTCATTCGGGAAGATAAATCCAGTGCGCTGGCCGAGCCA 2459 [	2460 CCTGCAITCAAAGCTTGGACCAGGGGTTCTTGTTCGGGAGGCAAAITTCCCTAGGAAAA 2519 [	2520 AGAAGACTTTTCTAATGTGGTCCAAATGCGGATCACTGGTCAGATGGATG	2580 GCACTGAGCTCCCTGTCTCTGGAAGTATTTAAGAAAAGGCTGGGCCAGGCACGATGGCTC 2639	2640 ACGCCTGTAATCCCCAGACTTTGGGAGGCCGAGGCGGGTCACCTGAGGTGAGGTT 2699	2700 TGAGAACAGCCTGGCCAACATGGTGAAACCTCATCTACTAAAAATACAAAAATTAGCC 2759 	2760 AGGCGTGGTGGCAGGTGCCTGTAATCCCAGCTACTTGGGAGGCTCAGGCATGAGAATCAC 2819 [	2820 TTANACCTGAGAGGCAGAGGTTACAGTGAGCCAAGATCGTGCCACTGCATTCCAGCCTGG 2879 2399 TTANACCAGAGAGGCAGAGGTTACAGTGAGCCAAGATCGTGCCACTGCATTCCAGCCTGG 2458	2880 GCGACAGAGCAAGACTCTGTCTCAAAAAAAAAAA 2917 	BC008736 2276 bp mRNA linear	N Homo sapiens ataxia, cerebellar, Cayman type (caytaxin), clone IMAGE:3162511), partial cds. BC008736.2 GI:38014014	Homo sapiens (human) SM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata		Klausner,R.D., Colling,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haleh,F.,
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				CAGAT	1320 CCCAGACTGCGTCCTGCAATACGAAGAGGAAAGACTGAAGGCCAGGAGGGAG	1380 GCCCCAGCCGGAGTTTGTGCTGCCCAGGTCTGAAGAAAACAGAAGTGGCACCAGTGGA 1439				GGTTCATCTCTGAAACCCAGCATCCTTTTCAGCTGCTTGAAACATTGTATTTTTTTT		1740 CACACTCACGAACTCTCAGCCGAGGAAGGCAAGAAGCGCAGGGGGTGGCCCGCGTGGGCGT 1799 	1800 CGGTGGCCTCCGCTCGCAGCCCCTGTGGTCAGAGCTGGATACAAGATTCAAGAC 1859 	1860 CCTTCTTGCTTGTCACCGGCTCCAGGTTGGAGCCACAGACACCCACGGCCACCGGGGC 1919	1920 TGGGTCTGGTCCTTTCCTGTGCCTTTCCTCCAGAATGCGGCCTCAGAACTC 1979 	1980 AACCCCCTATGAGGCCACGTCCTGGGGTAGCTCCTGACCTCGACCTTATGTCCAAAT 2039 	2040 TICACACCCAIGGITITICATITGACCCGCCCCTICTCGCTCATAATGACACCCAGCTC 2099 1619 TICACACCCAIGGITITICATITGACCCGCCCCTTCTCGCTCAIAATGACACCCAGCTC 1678	2100 CTTTGAGAGGATCAGAGCCCATTGCACAAGAAGAGCCGCTGCCAACCATCCTTGTCCTCC 2159

1312

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REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

JOURNAL PUBMED

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                                                                                  ACCAGATGATCGACCGGAGGTTGCGGAAAAACCTGAAGTCCTTGATCATCGTCCACCCCT
                                                                                                                    ACCAGATGATGATCGACCGGAGGTTGCGGAAAAACCTGAAGTCCTTGATCATCGTCCACCCCT
                                                                                                                                                                                                                                                                          ACAAGATCCAGTACGTGCACAGCTTGGAAGACCTGGAGCAACTCATCCCTATGGAACACG
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On Oct 28, 2003 this sequence version replaced gi:14250564.
On Oct 28, 2003 this sequence version replaced gi:14250564.
Contact: mGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.macymgcanhgri.nih.gov/
Contact: nisc.macymgcanhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakeley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gughca,J., Hadjighl,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantrippo,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton M., Soares M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ubdin, T.B., Tobiliyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunzatne, P.H., Richarde, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Hulyk, S.W., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LIAN at: http://image.llnl.gov Series: IRAL Plate: 5 Row: o Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TCTTCCTGTACGTCATCAGCAGCTTAGAGCTCCTGGTGGCTGAGGACTACATGATCGTGT
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/organism="Momo sapiens"

/mol_type="mRNA"

/db xref="taxon:9606"

/clone="IMAGE:3162511"

/clone_lib="NIH MGC 19"

/lab_host="NH MGC 19"

/note="Vector: poTB7"
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0; Mismatches
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Submitted (00-0CT-1999) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 134308)

BOR Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Londing (01-400-200) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Aug 1, 2002 this sequence version replaced gi:9256301.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.spic.stanford.edu

Quality: Phrap Quality >=40 100% of Sequence;

Bstimated Total Number of Errors is 0.
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Pred. No. 2.8e-272;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                            1. .134308
/organism="Homo sapiens"
/orlype="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
/clone="CT8-171N13"
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Best Local Similarity 99.8%;
Matches 1440; Conservative
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Homo sapiens chromosome 19 clone CTB-171N13, complete sequence
AC011488
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1 (bases I to 134308)

DOB Joint Genome Institute and Stanford Human Genome Center. Direct Submission
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 15 AC011488 LOCUS REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

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 11638.284 Million cell updates/sec Run on:

US-10-699-941-3 Title: Perfect score:

Scoring table: Sequence:

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4996997 seqs, 3332346308 residues

Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Score  2918	Query Match	Query Match Length DB	B 12	ID ADR16276	Description Adr16276 Human Cay
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420.4	14.4	485	0	ACH15328	Ach15328 Human adu
331.6	11.4	384	7	AAQ59527	Aag59527 Human bra

Detecting variant Cayman ataxia polypeptide or nucleic acid sequence in subject, by detecting presence or absence of variant Cayman ataxia

Adq21252 Human sof	Acc45236 Human BMC	Abl62307 Colon ade	Abl68862 Kidney ca		_	_	Abv27987 Human pro	Abv22147 Human pro	Human	Acn40083 Tumour-as	Adl39125 Human ova	Aah14059 Human cDN		Adl27146 Human gen	Ada03068 Human PPP	Adb72806 Human PPP	Ada66352 Human PPP	Continuation (3 of	Adq97183 Human can	Abd32769 Human can		Human	Human	Abal8915 Human ner
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330.4	327.6	318.2	318.2	318.2	315.8	302.2	302.2	302.2	259.2	245	243.6	243.4	242.2	241.8	241.8	241.8	241.8	241.6	240.8	240	239.6	239.6	239.6	239.2
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## ALIGNMENTS

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Human, jittery; 88; gene; Cayman ataxia; ATCAY; KIAA1872;
chromosome 19p13.3; ataxia; myoclonus; dystonia; epilepsy; nystagmus;
SNP; single nucleotide polymorphism.
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/standard_name= "Single nucleotide polymorphism"
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/product= "Cayman ataxia protein"
replace(1275,G)
                                                                                                                                             Location/Qualifiers
                ADR16276 standard; cDNA; 2918 BP.
                                                                                                                                                                                                                                                       03-NOV-2003; 2003US-00699941.
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08-NOV-2002; 2002US-0424973P.
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                                                                      Human Cayman ataxia cDNA.
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P-PSDB; ADR16277.
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RESULT 1
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or nucleic acid in biological

Claim 4; SEQ ID NO 3; 98pp; English.

The invention relates to detecting variant Cayman ataxia polypeptide or nucleic acid sequence (ATCAY) in a subject, involving providing a biological sample from a subject, where the biological sample comprises a cayman ataxia polypeptide or nucleic acid, and detecting the presence or absence of a variant Cayman ataxia polypeptide or nucleic acid in the biological sample. Also included is a kit comprising a reagent for absence of a variant Cayman ataxia nucleic acid or polypeptide in a biological sample. The human ATCAY gene (previously solated as cDNA KIAA1872, located on chromosome 19pl3.3) was identified or polypeptide in a biological sample. The human ATCAY gene (previously sen, located on mouse chromosome 10. The method is useful for detecting variant Cayman ataxia polypeptide or nucleic acid sequence in a subject. The presence of the variant Cayman ataxia, myoclonus, dystonia, epilepsy, and nystagmus in the subject. The biological sample; and an amiotic fluid sample, a tissue sample, urine sample, saliva sample; and an adult animal. The animal is a human. The human is an adult female of child-bearing age. The presence is the monding the contain the allele encoding the normal propertion or propertion or propertion. normal, non-disease causing protein. 

Sequence 2918 BP; 699 A; 868 C; 797 G; 554 T; 0 U; 0 Other;

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Best Local Similarity 100.0%;
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The invention relates to detecting variant Cayman ataxia polypeptide or nucleic acid sequence (ATCAY) in a subject, involving providing a biological sample from a subject, where the biological sample comprises a CC dayman ataxia polypeptide or nucleic acid in the presence of a variant Cayman ataxia polypeptide or nucleic acid in the cC dayman ataxia polypeptide or nucleic acid in the biological sample. Also included is a kit comprising a reagent for detecting the presence or absence of a variant Cayman ataxia nucleic acid or polypeptide in a biological sample. The human ATCAY gene (previously isolated as CDNA KIAA1872; located on chromosome 19p13.3) was identified or polypeptide in a biological sample. The human ATCAY gene (previously cor polypeptide on mouse chromosome 10. The method is useful for detecting variant Cayman ataxia polypeptide or nucleic acid sequence in a subject. The presence of the variant Cayman ataxia polypeptide or nucleic acid is indicative of a disorder chosen from ataxia, mycolonnia, cepilepsy, and nystagmus in the subject. The biological sample is chosen from allock sample, The subject is chosen from embryo, foetus, newborn amilotic fluid sample. The subject is chosen from embryo, foetus, newborn
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                                             Detecting variant Cayman ataxia polypeptide or nucleic acid sequence in subject, by detecting presence or absence of variant Cayman ataxia polypeptide or nucleic acid in biological sample.
2821 TAMACCTGAGAGGCAGAGGTTACAGTGAGCCAAGATCGTGCCACTGCATTCCAGCCTGGG
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chromosome 19p13.3; ataxia; myoclonus; dystonia; epilepsy; nystagmus;
SNP; single nucleotide polymorphism.
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373. .1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Cayman ataxia variant cDNA.
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cancer; cell proliferative disorder; gene;

15-OCT-2003; 2003WO-US029126. 18-OCT-2002; 2002US-0418988P.

WO2004060270-A2.

22-JUL-2004

Homo sapiens.

GENENTECH INC

WU T D. ZHOU Y.

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New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer

WPI; 2004-534300/51.

Zhou Y;

₩ TD,

Claim 1; SEQ ID NO 2457; 5504pp; English.

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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide concerneds (see SEQ ID Noi. to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80; sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described; (1) an expression vector comprising the above corporation to (a) a not concerned by any of the above comprising; (a) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising; (b) an amino acid sequence encoded by the full-comprising; (b) an amino acid sequences; or (c) a sequence of nucleotide sequences; (b) an amino acid sequences; or (c) a sequence comprising the above polypeptide full-length coding region of the above nucleotide sequences; or (c) a sequence comprising the above polypeptide full to (a) or (b); (5) a chimeric polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process or producing the above polypeptide; (8) an isolated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter contrained within the container and container and the container; (11) an article of manufacture comprising a container and the container; (12) methods of this above polyperide or TAT binding organic container and the container and the container.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the composition of matter contained within the containing the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth of presence of the above protein; (13) a method of protein defect of the above protein; (13) a method of protein of the apove protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopetide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer. The present sequence represents a
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Best Local Similarity 99.9
Matches 2915; Conservative
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human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;

Human tumour-associated antigenic target (TAT) cDNA sequence #2457.

(first entry)

07-OCT-2004

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ADQ85643;

ADQ85643 standard; cDNA; 4978 BP.

RESULT 3

ADQ85643

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Tumour-associated antigenic target (TAT) cDNA DNA326528, SEQ ID NO:5176.
                                                                                                                                                       Tumour-associated antigenic target; TAT; human; overexpression; cr
tumour; diagnosis; cell proliferative disorder; breast cancer;
colorectal cancer; lung cancer; ovarian cancer; liver cancer;
central nervous system cancer; bladder cancer; pancreatic cancer;
cervical cancer; melanoma; leukaemia; hybridisation probe;
chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                      gene therapy; cytostatic; gene; ss.
                             ACN40413 standard; cDNA; 4978 BP.
                                                                                             (first entry)
                                                                                            18-NOV-2004
                                                            ACN40413;
                ACN40413
RESULT
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cancer;

GAGGAATGGCAGGACGAAGATCTTCCCAGGCCACTCCCAGAAGAGACGGGGGTGGAACTG 480

421

29-SEP-2003; 2003WO-US028547.

WO2004030615-A2.

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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are oversyptessed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide esequences at least 80% identical to the TAT nucleic acids and polypeptides esequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptides, nucleic acids, and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with cancer, lung cancer, calcularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, carvical cancer, carvical cancer, orlorectal cancer, lung cancer, cervical cancer, pancreatic cancer, cervical cancer, pancreatic cancer, cervical cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence
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                                                                                                                                                                                   New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
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Pred. No. 0;
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Matches 2915, Conservative
                                                    (GETH ) GENENTECH INC.
                                                                                                                              WPI; 2004-347921/32.
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    Score 2896.6;
Pred. No. 0;
0; Mismatches
    99.3%;
Query Match
Best Local Similarity 99.8
Matches 2911; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genes and their expression products cloned from human cDNA libraries for treatment and diagnosis of diseases associated with their expression.
                                                                    GAGAACAGCCTGGCCAACATGGTGAAACCTCATCTTACTAAAAATACAAAAATTAGCCA
                                                                                                          GAGAACAGCCTGGCCAACATGGTGAAACCTCATCTAACAAAAATACAAAAATTAGCCA
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                                2645 GGCCTGTAATCCCAGACTTTGGGAGGCCGAGGCAGGCGGATCACCTGAGGTGAGGAGTTT
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WO200252005-A1

04-JUL-2002

Homo sapiens

06-SEP-2002

Human

ABN83973;

ABN8397

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424

TGTTTGCCA

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Sequence 4976 BP; 1241 A; 1417 C; 1366 G; 952 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143
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/pote= "This region is specifically claimed
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Matches 2890; Conservative
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P-PSDB; AAY70847.
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1461   CAGGTCTGAAGGCAGGGGGCACCAGTGGAAAACAGGTCTGGTCTCTGGTCTCTGGA   1460	1884 CAGGTTGGAGCCACAGACACCACCCCGCTGGGTTGCCTTTCCTGTGCC

complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 1'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence, where the combination of the 5'-end sequence 2'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in specification. The primers are useful for synthesising polynucleotides, gene therapy. The primers are useful for synthesising polynucleotides, the full-length cDNAs. The primers are also useful for the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and seally without any specialised methods. AMH0363 to AMH18628 and AMH18633 to AMH1862 represent human amino acid sequences; and AMH18629 to AMH1862 represent invarient invarient the semplification of the present invarient invarient the semplification of the present invarient invarient. 

Sequence 2894 BP; 677 A; 867 C; 798 G; 552 T; 0 U; 0 Other;

127 120 187 180 247 307 GGAGAGGCTGTCTCAGCTGCAGAGGGGTCATCCCTGCTTCAAGCCAGTGCCTCTTCCCAG 367 420 487 480 540 607 600 199. 99 CTCCCATGGGGACCACGAAGCCACGCTCCGGATGGAAAACGTGGACGTGAAGGAGGAAT 427 GCCCGGTGGAAGACACATCCTCCTCCCAACACGCTAAATTTCAACGGAGCGCATCGTA 547 AGACCCCCGATGAGACCGACTCGTGGAGTTCCTGGGGAATGGCAACGAACTGGAGTGGG 727 661 AGACCCCGATGAGACCGACTCGCTGGAGTTCCTGGGGAATGGCAACGAACTGGAGTGGG 720 9 68 GCCGATGAGAGGGGCGCAGCCCCCCCCCCCCCGCAGCCCCACCGCTAACCCTGCAC GGCGATGAGAGGGGGCGCAGCCCCGCGCTGGGGAGCCCACCGCTAACCCTGCAC CTCCCATGGGGACCACGCACGCTCCGGATGGAAACGTGGACGTGAAGGAGGAAT GGCAGGACGAAGATCTTCCCAGGCCACTCCCAGAAGAGACGGGGGTGGAACTGCTTGGCA 248 GGAGCGTGAGCGATGCCCAGCTGCACCCGGGCAGGGCTCGCCTTTGTTTTGCCAGTAAGGA TGCTGTCCGATGACTTCTTGGATACCCCTGATGACCTGGATATTAACGTGGATGACATCG CCCACCCACCCTGCACAAAAGAGCTGGCGGCGCTGGCCACGTCGCCCTGGGTGACCTT CCTCGGATGCAGAATCCGCCCCTGCGAGCATCCTCTTCCTCCTAGGCTCTGAAGGCCCGG GGCAGGACGAAGATCTTCCCAGGCCACTCCCAGAAGAGACGGGGGGGAACTGCTTGGCA GCCCGGTGGAAGACACATCCTCCTCCCAACACGCTAAATTTCAACGGAGCGCATCGTA AGAGGAAGACGCTGGTGGCCCCAGAGATCAACATTTCTCTGGATCAGAGTGAGGGGTCCC TGCTGTCCGATGACTTCTTGGATACCCCTGATGACCTGGATATTAACGTGGATGACATCG 541 AGAGGAAGACGCTGGTGGCCCCAGAGATCAACATTTCTCTGGATCAGAGTGAGGGGTCCC Gaps Length 2894; 1; 8; Indels DB 4; Score 2870.2; Pred. No. 0; 0; Mismatches 98.4%; Query Match
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ò	1268	TGCACAGCTTGGAAGACCTGGAGCAACTCCTATGGAACACGTCCAGATCCCAGACT 1327
qq	1260	TGCACAGCTTGGAAGACCTGGAGCAACTCATCCCTATGGAACACGTCCAGATCCCAGACT 1319
à	1328	GCGTCCTGCAATACGAAGAGGAAGACTGAAGGCCAGGAGGGGGGGG
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qq	1380	CGGAGTTTGTGCTGCCCAGGTCTGAAGAGAAGCCAGAGGTGGCACCAGTGGAAAACAGGC 1439
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Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
                                                                                                                                 Human; 88; gene; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; cancer; tumour.
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                                                         ADB62843 standard; cDNA; 2759
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28-MAR-2002; 2002EP-00007401.
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25-JAN-2002; 2002US-00350978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   as targets of gene therapy
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                              Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                       Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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The invention discloses a polymuclectide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel

CC polypeptides. Also claimed is a polypeptide encoded by the polymuclectide

or its partial peptide, an antibody binding to the polypeptide or peptide

of the polymuclectide, immunologically assaying the polypeptide or peptide

CC of the polymuclectide by contacting the polypeptide or peptide

CC with the antibody of the encoded protein, and observing the binding

CC with the antibody of the encoded protein, and observing the binding

CC with the antibody of the encoded protein, and observing the binding

CC with the antibody of the encoded protein, and observing the binding

CC contacting the polymuclectide. The polymuclectide in an expressible manner and an antisense polymuclectide. The oligomuclectide

CC detecting the polymuclectide. The polymuclectide, or as a probe

CC of detecting the polymuclectide. The polymuclectide and encoded

CC for detecting the polymuclectide. The polymuclectide and encoded

CC of genes may be included in them, for developing a diagnostic marker or

CC genes may be included in them, for developing a diagnostic marker or

CC gene may be included in them, for developing a diagnostic marker or

CC gene therapy. The genes are involved in tissue and/or cell

CC gene therapy. The genes are involved in tissue and/or cell

CC regeneration. Wembrane proteins, signal transduction-related proteins,

CC respectivity or expression of the encoded protein to treat diseases. The

CC neurological diseases, cancer, tumours. The cDNA may be used to regulate

CC the activity or expression of the envention. Note: Some of the sequence

CC data for this patent is not represented in the printed specification, but

<pre>// Match 10.04</pre>	2759 BP; 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;	based on semience information enumbled by the Durance Datont	
	tch  1 Similarity  1 Sinilarity  2 Si.24; Pred. No. 0;  1 Sinilarity  2 Si.24; Pred. No. 0;  2 Si.25; Conservative  2 Si.26; Conservative  3 Sindels  2 Conservative  3 Indels  2 Si.26; Conservative  4 Si.26; Conservative  5 Si.26; Conservative  6 Conservative  6 Conservative  6 Conservative  6 Conservative  7 Conservative  8 Corrected Conservative  8 Conservat	Technology   10   10   10   10   10   10   10   1	on sequence information supplied by the Buropean Patent Office.  2759 BP, 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;  89.04; Score 2599.2; DB 10; Length 2759;  6; Conservative 0; Mismatches 3; Indels 136; Gaps  CTCTGCCAGCCCTAAGCTGGGAAGAAGACACTACCTGGAGGGGGCGCAGGGGGGG  6GCGTTAAGAGGGGCCCAGCCCGCAGCCCCGCCTGAGGCGCGCAGGGGGGG  GGCGATGAGGGGGCCAGCCGCAGCCCGCGCTGGGAGGCCCAGGCGGGGGGGG
CTCTGCCAGCCCTGAGCTGCAGCAGCTACCTCGGAGGCGCGCGC	### 19.0#; Score 2598.2; DB 10; Length 2759; ####################################	Technology   Tec	Seed on sequence information supplied by the Buropean Patent Office.
CTCTGCCAGCCCTGAGCTGGAGCAGCTACCTCGGAGGCGCGCGC	### 19.0#; Score 2598.2; DB 10; Length 2759; ### 2186; Conservative	The control of con	Seed on sequence information supplied by the Buropean Patent Office.   11
CTCTGCCAGCCCTGAGCTGGAAGAAGCAGCTACCTCGGAGGCAGGC	### 10   10   10   11   11   11   11   1	Dec 2759 BP; 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;	Seed on sequence information supplied by the Buropean Patent Office.   10
CTCTGCCAGCCCTGAGCTGGAAGAAGCAGCTACCTCGGAGGCAGGC	### 189.0 0	10   10   10   10   10   10   10   10	Seed on sequence information supplied by the Buropean Patent Office.
CTCTGCCAGCCCTGAGCTGGAAGAAGCAGCTACCTCGGAGGGGGCGCGCAGGCGGGGGGGG	### 159, ### 1759;  ### 1519  ### 15	Comparison of the control of the c	nce 2759 BP; 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;  tch al Similarity 95.2½; Pred. No. 0; 2756; Conservative 0; Mismatches 1; Indels 136; Gaps 8 CTCTGCCAGCCCTGAGCTGGAGAGAGCAGGCGGGGGGGGG
CTCTGCCAGCCCTGAGCTGGGAAGAAGCAGCTACCTCGGAGGGGGCGCGCAGGGGGCGCGCGC	tch  39.0%; Score 2598.2; DB 10; Length 2759;  2156; Conservative 0; Mismatches 3; Indels 136; Gaps  8 CTCTCCCAGCCCTGAGCTGGGAGGAGCTACCTCGGAGGCGCGCGC	Conservative	Sed on sequence information supplied by the Buropean Patent Office.   1, 174 G; 517 T; 0 U; 0 Other;   1, 2759 BP; 654 A; 821 C; 747 G; 531 T; 0 U; 0 Other;   1, 2756;   1, 2
CTCTGCCAGCCCTGAGCTGGAAGAAGCAGCTACCTCGGAGGCGCGCAGGCGGCGCGCGC	tch  39.0%; Score 2598.2; DB 10; Length 2759;  2756; Conservative 0; Mismatches 3; Indels 136; Gaps  8 CTCTCCAGCCCTGACCTGACAGAAGAAGACACTACCTCGAAGACGCGCAGGCGGC 67  1 CTCTCCCAGCCCTGAACTGACAGAAGAAGACACTCCGGAAGACGCGCAGGCGGC 60  68 GCCGATGAAGAGACAGAAGAAGACACTCTCCTCGAAGACCCCACCTCACCTCCTC 12  61 GGCGATGAAGAGGGGCGCAGCCCCCGCGCTCGAGGCCGCAGGCGGC 60  68 GCCGATGAAGAGGGGCGCAGCCCCCGCGCTCGGAGGCCCACCTCTCCTC 12  61 GGCGATGAAGAGGGGCGCAGCCCCCGCGCTCGCGCAGGCCCCCCCTCCTCCTCT 18  121 CCCACCCCACCCCCCCCCCCCCCCCCCCCCCCCCCC	10   10   10   10   10   10   10   10	Sed on sequence information supplied by the Buropean Patent Office.   Sec
CTCTGCCAGCCCTGAGCTGGGAAGAAGCAGCTACCTCGGAGGGAG	### 159.0%; Score 2598.2; DB 10; Length 2759; ####################################	10   10   10   10   10   10   10   10	Sed on sequence information supplied by the European Patent Office.   Sed on sequence information supplied by the European Patent Office.   Sed of Secre 2598.2; DB 10; Length 2759; all Similarity 95.2%; Pred. No. 0; all Simi
CTCTGCCAGCCCTGAGCTGGAAGAAGCAGCTACCTCGGAGGCAGGC	tch  39.0%; Score 2598.2; DB 10; Length 2759; 2756; Conservative  0; Mismatches  8 CTCTCCCAGCCCTGAGCTGGAAGAGCAGCAGCGGGGGGG  1 CTCTCCAGCCCTGAGCTGGAAGAGCAGCAGCGGGGGGGGG	10   10   10   10   10   10   10   10	Sed on sequence information supplied by the Buropean Patent Office.   Care 2759 BP; 654 A; 821 C; 747 G; 537 T; 0 U; 0 other;   Care 2759 BP; 654 A; 821 C; 747 G; 537 T; 0 U; 0 other;   Care 2598.2; DB 10; Length 2759;   Secretarive
CTCTGCCAGCCCTGAGCTGGAAGAAGCAGCTACCTCGGAGGCAGGC	tch  39.0%; Score 2598.2; DB 10; Length 2759; 2756; Conservative 0; Mismatches 3; Indels 136; Gaps  8 CTCTCCCAGCCCTGAGCTGGAGGAGGAGGCGGGGGGGGGG	10   10   10   10   10   10   10   10	Sed on sequence information supplied by the Buropean Patent Office.   Carbor   Sed A; 821 C; 747 G; 537 T; 0 U; 0 Other;     Sed A; 821 C; 747 G; 537 T; 0 U; 0 Other;     Sed A; 821 C; 747 G; 537 T; 0 U; 0 Other;     Sed A; 821 C; 747 G; 537 T; 0 U; 0 Other;     Sed A; 821 C; 747 G; 537 T; 0 U; 0 Other;     Sed A; 821 C; 747 G; 537 T; 0 U; 0 Other;     Sed A; 821 C; 747 G; 537 T; 0 U; 0 Other;     Sed A; 821 C; 747 G; 537 T; 0 U; 0 Other;     Sed A; 821 C; 747 G; 537 T; 0 U; 0 Other;     Carbor Cacaca Caca
CTCTGCCAGCCCTGAGCTGGAAGAAGCAGCTACCTCGGAGGCAGGC	tch al Similarity 95.2%; Pred. No. 0; 2756; Conservative 0; Mismatches 3; Indels 136; Gaps 8 CTCTGCCAGCCCTGAGCTGGAAGAAGAGCAGCCGGCGCGCGC	10   10   10   10   10   10   10   10	Sed on sequence information supplied by the European Patent Office.   Sed 2759 BP; 654 A; 821 C; 747 G; 537 T; 0 U; 0 other;   Cth
CTCTGCCAGCCCTGAGCTGGAAGAAGCAGCTACCTCGGAGGCAGGC	tch  1 Similarity  1 S.24; Pred. No. 0;  2756; Conservative  2 Mismatches  2 TCTCCCAGCCCTGAGCTGGAGGAGCAGGCGGGGGGGGGG	10   10   10   10   10   10   10   10	Sed on sequence information supplied by the Buropean Patent Office.   Care 2759 BP, 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;   Care 2759 BP, 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;   Care 259 BP, 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;   Care 259 BP, 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;   Care 259 BP, 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;   Care 259 BP, 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;   Care 250 BP, 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;   Care 250 BP, 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;   Care 250 BP, 654 A; 821 C; 747 G; 821 G; 822 G
CTCTGCCAGCCCTGAGCTGGAAGAAGCAGCTACCTCGGAGGCAGGC	tch  1 Similarity  1 S.2%; Pred. No. 0;  2756; Conservative  2 Mismatches  2 Tridela 136; Gaps  2 Creccadecceranderagandanderaceraceraganderag	10   10   10   10   10   10   10   10	Sed on sequence information supplied by the Buropean Patent Office.   Sequence information supplied by the Buropean Patent Office.   Conservative   Sequence 2598.2; DB 10; Length 2759; al Similarity   S5.2%; Pred. No. 0; a.y. Indels 136; Gaps   Similarity   S5.2%; Pred. No. 0; a.y. Indels 136; Gaps   CTCTGCCAGCCCTGAGCTGAGAGAGACTACCTCGGAGGCGCGCAGGCGCGCGC
CTCTGCCAGCCCTGAGCTGGGAAGAGCAGCTACCTCGGAGGCAGGGCGCGCAGGGGCGCCAGGGGGCGCGCGGGGCGCGCGGGGCGCGCGGGGCGCGCGGGG	tch al Similarity 95.2%; Pred. No. 0; 2756; Conservative 0; Mismatches 3; Indels 136; Gaps 8 CTCTGCCAGCCCTGAGCAGAAGAAGAGCAGCAGGCGGGGGGGG	Colored Colo	Sed on sequence information supplied by the Buropean Patent Office.   Care 2759 BP; 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;   Care 2598.2; DB 10; Length 2759;   Care 2508.2; Pred. No. 0;   Care 2508.2; DB 10; Length 2759;   Care 2508.2; Pred. No. 0;   Care 2508.2; DB 10; Length 2759;   Care
CTCTGCCAGCCCTGAGCTGGGAAGAAGCAGCTACCTCGGAGGCAGGC	tch al Similarity 95.2%; Pred. No. 0; 2756; Conservative 0; Mismatches 3; Indels 136; Gaps  8 CTCTGCCAGCCCTGAGCTGGAAAGAGCAGCTCCGGAGGCGGCGCGCGC	Colored Colo	Sed on sequence information supplied by the European Patent Office.   Sed 8; 554 8; 51 C; 747 G; 537 T; 0 U; 0 Other;   Conservative   Sec. 2598.2; DB 10; Length 2759;   Sec. 2598.2; DB 10; Length 2759;   Sec. 256; Conservative   O; Mismatches   3; Indels 136; Gaps   CTTGCCAGCCTGAGCTGAGAGAGAGAGAGCTGCTGGAGGCGGGGGGGG
CTCTGCCAGCCTGAGCTGGGAAGAGCGGCTACCTCGGAGGCAGGGGGGCGCGGGGGCGGGC	tch  39.0%; Score 2598.2; DB 10; Length 2759; 2756; Conservative 0; Mismatches 3; Indels 136; Gaps  8 CTCTCCCAGCCCTGAGCTGGGAGAGAGAGCAGGCAGGCAG	10	Sed on sequence information supplied by the Buropean Patent Office.   Ince 2759 BP; 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;   Ltch
CTCTGCCAGCCCTGAGCTGGGAAGAGCGGCTACCTCGGAGGCAGGC	tch al Similarity 95.2%; Pred. No. 0; 2756; Conservative 0; Mismatches 3; Indels 136; Gaps 2756; Conservative 0; Mismatches 3; Indels 136; Gaps 8 CTCTGCCAGCCCTGAGCTGGGAAGAAGCTACCTCGGAGGCAGGGCGCGCAGGCGGGGGGGG	nce 2759 BP; 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;  tch	Sed on sequence information supplied by the Buropean Patent Office.   Ince 2759 BP; 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;   Lth   S9.0%; Score 2598.2; DB 10; Length 2759; al Similarity 95.2%; Pred. No. 0; 2756; Conservative 0; Mismatches 3; Indels 136; Gaps 8 CTCTGCCAGCCCTGAGCTAGCAGAGCAGCCGGGGGGG 67
CTCTGCCAGCCCTGAGCTGGGAAGAAGCAGCTACCTCGGAGGGAG	tch al Similarity 95.2%; Pred. No. 0; 2756; Conservative 0; Mismatches 3; Indels 136; Gaps 2756; Conservative 0; Mismatches 3; Indels 136; Gaps 8 CTCTGCCAGCCCTGAGCTGGGAAGAGAGCTACCTCGGAGGCAGGGCGCGCAGGCGGGCG	nce 2759 BP; 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other; tch 89 0%; Score 2598.2; DB 10; Length 2759; al Similarity 95.2%; Pred. No. 0; 2756; Conservative 0; Mismatches 3; Indels 136; Gaps 8 CTCTCCCAGCCCTGAGCTGGGAAGAGAGCTGCCTCGGAGGCGGGGCGCGGGGGGGG	Sed on sequence information supplied by the Buropean Patent Office.   Sed B; 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;   Lth
CTCTGCCAGCCCTGAGCTGGGAAGAAGCAGCTACCTCGGAGGCAGGC	tch al Similarity 95.2%; Pred. No. 0; 2756; Conservative 0; Mismatches 3; Indels 136; Gaps 8 CTCTGCCAGCCTGAGAAGAAGAGACTACCTCGGAGGAGGAGGGCGCGCAGGCGGC 67	nce 2759 BP; 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other; tch al Similarity 95.2%; Pred. No. 0; 2756; Conservative 0; Mismatches 3; Indels 136; Gaps 8 CTCTGCCAGCCTGAGCAGAAGCAGCTACCTCGGAGGCAGGC	sed on sequence information supplied by the European Patent Office.  nce 2759 BP; 654 A; 821 C; 747 G; 537 T; 0 U; 0 Other;  tch al Similarity 95.2%; Pred. No. 0; 2756; Conservative 0; Mismatches 3; Indels 136; Gaps 8 CTCTGCCAGCCTGAGCAGAAGAAGAACCAGGAGAGCAGGCGGCAGCGCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCCGCAGCCGCAGCCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCGCAGCCCGCAGCCGCAGCCCCCC
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1087 1147 1004 1207 1064 1267 1124 1327 1184 1387 1244 1447 1304 1807 1605 CGAACTCTCAGCCGAGGAAGGCAAGAAGCGCAGGGGTCGCCCGCGTGGCGTCGGTGGCC 1664 CATGGTTTTTCATTTGACCCCCCTTCTCGCTCATAATGACACCCAGCTCCTTTGAGA 2107 884 944 1208 CTGTGCTGGCCATCTCGCCCTTTCATCAGGTCAAGTTCATCAACAAGATCCAGTAGG 1268 TGCACAGCTTGGAAGACCTCGGACTCATCCCTATGGAACACGTCCAGATCCCAGACT 1088 CGCCCCGGCGGAGGATGCCTGGAATCGGCTGAAGAAGAGTGCTACCAGATGATCGACC 1388 CGGAGTTTGTGCTGCCCAGGTCTGAAGAGAGCCAGAGGTGGCACCAGGTGGAAAACAGGT 1245 CGGAGTTTGTGCTGCCCAGGTCTGAAGAGAAGCCAGAGGTGGCACCAGTGGAAAAACAGGT CGAACTCTCAGCCGAGGAAAGGCAAAGAAGCGCAGGGGGGGCCCCGCGTGGCGTCGGTGGCC 1748 1808 2048

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CTTCCCAGCTCCCATGGGGACCACCGAAGCTCCGGATGGAAAACGTGGACGTGAA 120
                                                                                                                                                                                                                                                                                               dementia and various cancers,
                                                                                                                                                                                                                                                                                                                                                The invention relates to 2495 novel polynucleotides (I) and their encode polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% or 90% identity the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a nucleotide sequence of the invention.
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                                                                                                                                                                                                                                                                               Novel 2495 cDNA, useful for treating osteoporosis, neurological Alzheimer's diseases, Parkinson's diseases, dementia and various
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Pred. No. 0;
0; Mismatches
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Nagai K,
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95.2%;
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09-MAY-2003; 2003JP-00131392.
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Isono Y,
                                                                                                                                                                                                                                       2004-535376/52.
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                    Homo sapiens
                                              EP1440981-A2
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Yamamoto J,
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CATGGTTTTTCATTTGACCCGCCCCCTTCTCGCTCATAATGACACCCCAGCTCCTTTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                  GACTITICTAATGTGGTCCAAATGCGGATCACTGGTCAGATGGACTCTAGAAGCACTGAG
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                                            AATGACACCCCAGTAATCTAGAACATTCTCAAGCCCCTTTAACTCAGATGTCAAGCCACC
                                                                                                                                                                                           CAACCCAGCGTCAGGCTGGGACACGCCAACGCTGTTCCGGGTTGGAACAGCAGAGGCTCA
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                                                                                                                                                                                                                                                                             GAPACTGGCTCTGAAATAGGCAGACCTAGCAAGAGGAAGATACAGGGTATCGGGCGTTTG
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                                                                                                                                     GGGCADACCCCGTCADACCTCCCACCAAGGAATGAGATATGTGGACCTCACTGCTCCCC
                                                                                                                                                     CTCCCTGTCTCTGGAAGTATTTAAGAAAAGGCTGGGCCAGGCACGATGGCTCACGCCTGT
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                                                                                                    GAAACTGGCTCTGAAATAGGCAGACCTAGCAAGAGGAAGATACAGGGTATCGGGCGTTTG
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The invention relates to detecting variant Cayman ataxia polypeptide or nucleic acid sequence (ATCAY) in a subject, involving providing a biological sample from a subject, where the biological sample comprises a Cayman ataxia polypeptide or nucleic acid, and detecting the presence or absence of a variant Cayman ataxia polypeptide or nucleic acid in the biological sample. Also included is a kit comprising a reagent for chicogracial sample and part of a presence or absence or absence of a variant Cayman ataxia nucleic acid or polypeptide in a biological sample. The human ATCAY gene (previously isolated as cDNA KIAABT2, located on chromosome 19p1) 3) was identified and mapped using the fact that it is the homologue of the mouse jittery gene, located on mouse chromosome 10. The method is useful for detecting variant cayman ataxia polypeptide or nucleic acid sequence in a subject. The presence of the variant Cayman ataxia polypeptide or nucleic acid sample. The presence of the variant Cayman ataxia, myoclonus, dystonia, complete acid sample, a tissue sample, urine sample, saliva sample, and an amincit from blood sample, and an adult animal. The submit is a human. The animal is a human. The human is an adult female of child-baring age. The present sequence is the DNA representing a Human ATCAY splice site of exon 9-introm of canner a read through mirtain represent to be produced.
                                                                                                                                                                            Human; jittery; ds; Cayman ataxia; ATCAY; KIAA1872; chromosome 19p13.3; ataxia; myoclonus; dystonia; epilepsy; nystagmus; splice site mutant; SNP; single nucleotide polymorphism.
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49.3%; Score 1438.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches
                                                                                                                                     Human Cayman ataxia splice site mutant DNA
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                    ADR16283 standard; DNA; 47219 BP
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                  13720 CTAGCATGTCCTGAGGCGACGTGAGCATAACAAAGGACATGGAAGATTCCAGATGCC
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                                                                                           AATCTTCCAAGGGTGCCAGCCCCTCCGTTCATCTCTGAAACCCAGCATCCTTTTCAGCTG
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The invention relates to detecting variant Cayman ataxia polypeptide or nucleic acid sequence (ATCAY) in a subject, involving providing a biological sample from a subject, where the biological sample comprises a cayman ataxia polypeptide or nucleic acid, and detecting the presence or absence of a variant Cayman ataxia polypeptide or nucleic acid in the biological sample. Also included is a kit comprising a reagent for detecting the presence or absence of a variant Cayman ataxia nucleic acid or polypeptide in a biological sample. The human ATCAY gene (previously isolated as CDNA KIAA172, located on chromosome 19p13.3) was identified and mapped using the fact that it is the homologue of the mouse Jittery gene, located on mouse chromosome 10. The method is useful for detecting variant Cayman ataxia polypeptide or nucleic acid sequence in a subject. The presence of the variant Cayman ataxia polypeptide or nucleic acid is indicative of a disorder chosen from ataxia, myoclonus, dystonia, epilepsy, and nystaguus in the subject. The biological sample is chosen from blood sample, a tissue sample, urine sample, saliva sample, and an aminatic fluid sample. The subject is chosen from enbryo, foetus, newborn animal; and an adult feman adult animal. The animal is a human. The human genomic DNA for ATCAY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1475 CAAGCATGTCCTGAGGCGACGTGAGCATAACAAAGGACATGGAAGAAGATTCCAGATGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
49.3%; Score 1438.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches
Claim 4; SEQ ID NO 11; 98pp; English
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The invention discloses a polymucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel

CC from 1970 fully defined nucleotide sequences which encode novel

CC polypoptides. Also claimed is a polypoptide encoded by the polymucleotide or peptide or its partial peptide, immunologically assaying the polypoptide or peptide or the polymucleotide. Immunologically assaying the polypoptide or peptide of the polymucleotide by contacting the polymucleotide or peptide or the encoded protein, and observing the binding between the two, a transformant carrying the polymucleotide in an expressible manner and an antisense polymucleotide. The oligonucleotide is useful as a primer for synthesising the polymucleotide and encoded for detecting the polymucleotide. The polymucleotide and encoded contacting the polymucleotide and many disease-related contacting the polymucleotide. The polymucleotide and encoded contacting the polymucleotide in the many be included in their expression and activity, or as targets of genes may be included in their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, disease-related proteins are coding them can be used as indicactors for diseases (e.g. osteoporosis, encoding them can be used as indicactors for diseases (e.g. osteoporosis, encoding them can be used as indicactors for diseases (e.g. osteoporosis, encoding them can be used as indicactors for diseases (e.g. osteoporosis, encoding them can be used as indicactors for diseases (e.g. osteoporosis, encoding them can be used as indicactors for diseases (e.g. osteoporosis, encoding them can be used as indicactors for diseases (e.g. osteoporosis, encoding them can be used as indicactors for diseases (e.g. osteoporosis, encoding them can be used as indicactors for diseases (e.g. osteoporosis, encoding the printed specification, but the printed specification, but the printed specification, but the sequence presented is a cDN
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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACGATGCAGTATTTGTGCGTTCCAGAAAAGGCCCCAGCTCTGAGCCCCTCACCTTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1325.8; DB 10; Lengt
Pred. No. 3.8e-313;
0; Mismatches 2; Indels
                                                                                          /product= "Clone OCBBF20001780 protein"
                    Location/Qualifiers
1990. .2334
/*tag= a
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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P-PSDB; ADB64802.
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Best Local Similarity
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                                                                                                                                                                                                      AAGGAATGAGATATGTGGACCTCACTCCCCCCAACCCAGCGTCAGGCTGGGAACACCCC
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CCGCTGCCAACCATCCTTGTCCTCCGATTGCAAAATGACACCCCAGTAATCTAGAACATT
                                                                                                                                                                                                                                                                 AACGCTGTTCCGGGTTGGAACAGCAGAGGCTCAGAAACTGGCTCTGAAATAGGCAGACCT
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                                                                                     CTCAAGCCCCTTTAACTCAGATGTCAAGCCACCGGGCAAACCCCGTCAATACCTCCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA encoding clone OCBBF20001780.
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Mouse; jittery; ss; gene; Cayman ataxia; ATCAY; KIAA1872; chromosome 10; ataxia; myoclonus; dystonia; epilepsy; nystagmus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting variant Cayman ataxia polypeptide or nucleic acid sequence in subject, by detecting presence or absence of variant Cayman ataxia polypeptide or nucleic acid in biological sample.
   2545 AAACCTGAGAGGCAGAGGTTACAGTGAGCCAAGATCGTGCCACTGCATTCCAGCCTGGGC
                                                                                                                                                                                                                                                            /*tag= a
/product= "Jittery"
/transl_except= (pos:1044. .1046,aa:Glu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 1; 98pp; English.
                                             2605 GACAGAGCAAGACTCTGTCTC 2625
                                 2882 GACAGAGCAAGACTCTGTCTC 2902
                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                     ADR16274 standard; cDNA; 2166
                                                                                                                                                                                                                                                                                                                                          03-NOV-2003; 2003US-00699941.
                                                                                                                                                                                                                                                                                                                                                            01-NOV-2002; 2002US-0422971P.
08-NOV-2002; 2002US-0424973P.
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/*tag= a
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P-PSDB; ADR16275.
                                                                                                                                                                 Mouse jittery cDNA.
                                                                                                                                                                                                                                                                                                   US2004146900-A1
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                                                                                                                                                                                                                   Mus musculus
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                                                  GCCACCGGGCAAACCCCGTCAATACCTCCCAACGAATGAGATATGTGGACCTCACTG
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The invention relates to detecting variant Cayman ataxia polypeptide or nucleic acid sequence (ATCAY) in a subject, involving providing a biological sample from a subject, where the biological sample comprises a CC Cayman ataxia polypeptide or nucleic acid, and detecting the presence or absence of a variant Cayman ataxia polypeptide or nucleic acid in the cological sample. Also included is a kit comprising a reagent for detecting the presence or absence of a variant Cayman ataxia nucleic acid or polypeptide in a biological sample. The human ATCAY gene (previously isolated as cDNA KIAA1872, located on chromosome 19p13.3) was identified or mousped using the fact that it is the homologue of the mouse Jittery gene, located on mouse chromosome 10. The method is useful for detecting variant Cayman ataxia polypeptide or nucleic acid sequence in a subject. CC The presence of the variant Cayman ataxia polypeptide or nucleic acid sequence in a disorder chosen from ataxia, mycolonus, dystonia, cpilepsy, and nystagmus in the subject. The biological sample, and an acid is from blood sample, a tissue sample, urine sample, saliva sample, and an andult female of child-bearing age. The present sequence is the coby animal, young animal, and an adult animal. The animal is a human. The human is an adult female of child-bearing age. The present sequence is Sequence 2166 BP; 523 A; 619 C; 576 G; 448 T; 0 U; 0 Other; us-10-699-941-3.rng

1073 ACCTGAACGGTGCCCCGGGGGAGGATGGCTGGAATCGGCTGAAGAAGTGCT 1132	Qy         1253 ACAAGATCCAGTACGTGCACAGCTTGGAAGACCTGGAGCAACTCATTGGAACACG         1312           Db         1258 GTAAAATTCAGTACGTGCACAGCTGGAGGGACTGATTCCCATGGAACACG         1317           Qy         1313 TCCAGATCCCAGCTGCAATACGAAGAGAAGACTGAAGACCGAGGAGGAGA         1372           Db         1318 TGCAGTCCTGCCATTACGAAGACTGAAGACTCCGAGGAGGAGA         1372           Db         1318 TGCAGCTGCCTGCCATTACGAAGACTCCGAGCCAAGAGGCAAGAGACTCCGAGGCAAGAGAGAG	Oy 1373 GCGGAGGCCCCAGCCGGAGTTTGTGCTGCCCAGGTCTGAAGAGAGAG	Qy         1490 GCGACGTGAGCATAACAAAGGACATGGAAGAATTCCAGATGCCAGAAAACCTCTGTCA 1549           Db         1498 CTACCCAGAACCTAGACATGGACAGAGATTATTCCCAACATCATGTAACCCTCATCC 1554           Qy         1550 GACGCCCACTGGCCCCAGATCTCATCCTGCCTCATCC 1586           Db         1555 GAAGCCCTGGAGCCCCGCCTTCATCGAGCCTCCACC 1591	RESULT 14 AAH08588 ID AAH08588 standard; cDNA; 790 BP. XX AC AAH08588;	AX 26-JUN-2001 (first entry) XX DE Human cDNA clone (5'-primer) SEQ ID NO:5423. XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; 88. XX XX XX XX XX	EP107 07-FF	PR 29-JUL-1999; 99JP-00248036. PR 27-AUG-1999; 99JP-00300253. PR 11-JAN-2000; 2000JP-00118776. PR 02-MAY-2000; 2000JP-0018767. PR 09-JUN-2000; 2000JP-00241899. XX	PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J; PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T; XX XX DR WPI; 2001-318749/34. XX Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y
	184 CCTTCCTCGGATGCAGATCGCCCCTGCGAGCATCCTCTTCCTCCTAGGCTCTCAGGCGC 2	DECENTICACCAGGCCCTTGGCTTGGGTACCATCGAGAAATGCCCGCCTTTGTGTCCAGGTG 297	ACGTGAAGGAGGAATGGCAGGACGAAGATCTTCCCAGGCCACTCCCAGAAGAGAGGGGGGGG		Db   598   AAAGCGAGGGCTTCTGCACGACGACTCCTCGATGACACGCACACTGATGACATGACATCA   657			Qy         953 TCGCAGCTTCCTTCCAGACAGCAGCTCCCCGACTACCACTACATCATGGAGAACC         1012           Db         958 TTGCAGCTTCCTGCCAGATAGCAGCTCCCCAGACTATCATGAGAAATC         1017           Qy         1013 TCTTCCTGTACGTCATCAGCAGCTTAGAGCTCCTGGTGGCTGAGGACTACATGATCGTGT         1072           Db         1018 TCTTCCTGTACGTCATCAGCAGCTTAAACTGCTCGTGGCTGAGGACTACATGATCGTGT         1077

Tue Mar

The present invention describes primer sets for synthesising 5602 fulllength cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the comprising a sequence complementary to the comprise and an oligonucleotide comprising a sequence complementary to a sequence and an oligonucleotide comprises a 3'-end sequence complementary to a coligonucleotide which comprises a 3'-end sequence of polynucleotide which comprises a 1'-end sequence, where the coligonucleotide comprises a 1'-end sequence of in the comprise of the polynucleotide and the combination of the 5'-end sequence 1'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in specification. The primer sets can be used in seful for the perturbance of the full-length cDNAs. The primers are also useful for the comprise and of actionable of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are primers and MAH13629 to AAH13628 and AAH13633 to AAH13632 represent human amino acid sequences; and ANH3629 to AAH13622 represent invention of the present invention of the present invention of the present invention allost which are used in the exemplification of the present invention and perturbance and and an are used in the exemplification of the present invention. Claim 1; SEQ ID NO 5423; 2537pp + Sequence Listing; English. present invention 

Sequence 790 BP; 166 A; 245 C; 251 G; 125 T; 0 U; 3 Other;

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247 307 367 487 GCCCGGTGGAAGACACATCCTCCTCCCAACACGCTAAATTTCAACGGAGCGCATCGTA 547 AGAGGAAGACGCTGGTGGCCCCCAGAGATCAACATTTCTCTCGGATCAGAGTGAGGGGTCCC 607 9 CTCGGATGCAGAATCCGCCCCTGCGAGCATCCTCTTCCTCCTAGGCTCTGAAGGCCCGG CTCTGCCAGCCCTGAGCTGGGAAGAAGCAGCTACCTCGGAGGCAAGGCGCGCAAGGCGCGC GGCGATGAGAGGGGGCAGCCGCAGCCCCGCGCTGGGGAGCCCCACCGCTAACCCTGCAC 248 GGAGCGTGAGCGATGCCCAGCTGCACCCGGGCAGGGCTCGCCTTTTGTTTTGCCAGTAAGGA GGAGAGGCTGTCTCAGCTGCAGAGGGGTCATCCCTGCTTCAAGCCAGTGCCTCTTCCCAG CCCACCCACCCTGCACAAAGAGCTGGCGGGCGCTGGCCACGTCGCCCTGGGTGACCTT CCTCGGATGCAGAATCCGCCCTGCGAGCATCCTCTTCCTCCTAGGCTCTGAAGGCCCGG GGCAGGACGAAGATCTTCCCAGGCCACTCCCAGAAGAGACGGGGGGTGGAACTGCTTGGCA Gaps 1; 4; Length 790; 5; Indels Score 745.2; DB 4; Pred. No. 1.5e-171; 0; Mismatches 5; 25.5%; Best Local Similarity 75.2 Matches 758; Conservative 128 308 368 361 æ 68 19 188 181 428 488 548 ð. 셤

99 727 601 TGCTGTCCGATGACTTCTTGGATACCCCTGATGACCTGGATATTAACGTGGATGACATCG 668 AGACCCCCGATGAGACCGACTCGCTGGAGTTCCTGGGGAATGGCAACGAACTGGAGTGGG 608 IGCIGICCGAIGACTICTIGGAIACCCCTGAIGACCIGGAIATIAACGIGGAIGACAICG Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss. 728 AAGACGACCCCCGTGGCCACC-GCCAAGAACATGCCCGGGGA 770 DNA encoding novel human diagnostic protein #16127. AAS80323 standard; cDNA; 703 BP 30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. Tang YT; 13-FEB-2002 (first entry) WPI; 2001-639362/73. P-PSDB; ABG16136. Drmanac RT, Liu C, (HYSE-) HYSEQ INC. WO200175067-A2 Homo sapiens. 11-OCT-2001. AAS80323; RESULT 15 AAS80323 셤 ò 셤 ઠે 

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ ID NO 16127; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed confin diagnostics as expressed sequence tags for identifying expressed confin diagnostics of the creation of the confine co

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               Query Match 23.1%; Score 675; DB 5; Length 703; Best Local Similarity 98.4%; Pred. No. 2e-154; Matches 692; Conservative 0; Mismatches 10; Indels
Sequence 703 BP; 152 A; 218 C; 213 G; 120 T; 0 U; 0 Other;
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239	239	239	238.8	238.8	238.6	238.6	238.4	238.4	238	238	238	238	238	238	237.8	237.8	237.8	237.8	237.8	237.8
22	56	27	28	53	30	31	32	33	34	35	36	37	38	30	40	41	42	43	44	45
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## ALIGNMENTS

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         Sequence 1, Application US/09174937
Sequence 1, Application US/09174937
Patent No. 6756212
GENERAL INFORMATION:
APPLICANT: Knodadoust, Mehran
TITLE OF INVENTION: Homology to NIP2 Proteins and Uses Thereof
TITLE OF INVENTION: Homology to NIP2 Proteins and Uses Thereof
TITLE OF INVENTION: Homology to NIP2 Proteins and Uses Thereof
TITLE OF INVENTION: HOMOLOGY to NIP2 Proteins and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/174,937
CURRENT FILING DATE: 1998-10-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 1
LENGTH: 3076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 CTGGGAAGAAGCAGCTACCTCGGAGGCAGGCGCGCGCGGCGGCGGCGATGAGAGGGGGC
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99.0%; Score 2887.6;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2890; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KBY: CDS
; LOCATION: (370)..(1482)
US-09-174-937-1
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ORGANISM: Homo sapiens
US-09-174-937-1
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201 CGCCCCTGCGAGCATCCTCTTCCTAGGCTCTGAAGGCCCGGGGAGCGTGAGCGATGC

264 CCAGCTGCACCCGGCCAGGGCTCGCCTTTGTTTGCCAGTAAGGAGGAGAGGCTGTCTCAG 323 

324 CTGCAGAGGGGTCATCCCTGCTTCAAGCCAGTGCCTCTTCCCAGGCTCCCATGGGGACCAC 383

Oy         308 GGAGAGCTGTCTCAGCTGCAGAGGGTCATCCTGCTTCAAGCCAGTGCCTTTCCCAG         367           Db         231 GGAGAGCTGTCTCAGCTGCTTCCAGCTGCTTCCCAG         290           Oy         368 CTCCATGGGGGACCACGCTCCGGATGGAAACGTGGAGGAGAAA         427           Db         291 CTCCATGGGGACCACCCAGCTCCGGATGGAAAACGTGGAGGAAA         350           Oy         428 GGCAGGACGAAGCCACGCTCCGGATGGAAAACGTGGAGGAAA         350           Oy         428 GGCAGGACGAAGCCACGCCACAGCCCCCAGAAAACGTGGAAACGTGAAGGAAAACGTGGAAACGTGGAAACGTGGAAACGTGGAAAACGTGGAAACGTGGAAACGCTGCAAGAAACGTGGAAACGCTGAAGAAACGTGGAAACGCTGCAAGAAACGTGGAAACGCTGCAAGAAACGTGGAAACGCTGCAAGAAACGTGGAAACGCTGCAAGAAACGCTACCCAAAAAACGTGGAAACGCTGCAAAAACGTGGAAACGCTACCCAAAAAACGTGGAAACGCAACGCACCTCCCAAAAAACGTGGAAACGCTGCAAAAACGTGGAAACGCTGCAAAAACGTGGAAAACGTTGGAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAACGTTGGAAAACGTTGGAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAACGTTGGAAAACGTTGGAAAACGTTGGAAAACGTTGGAAAAACTTGCTTG	40000	DD		Qy         908         CCCACGAGGGGAACTACGGCGAAGGCCTCAACGCCATCATCGTCTTCGCAGCCTGCTTCC         967           Db         765         CCCACGAGGGTACTACGGCGAAGGCCTCAACGCCATCATCGTCTTCGCAGCCTGCTTCC         824           Qy         968         TTCCAGACAGCCTCCCCGGACTACCACTACATGGAGAACCTCTTCCTGTACGTCA         1027           Db         825         TTCCAGACAGCCTCCCCGAACTACCACTACATGGAGAACCTCTTCCTGTACGTCA         884	1028 885 1088 945	0y         1148         GGAGGTTGCGGAAAAACCTTGATCATCGTCCCCCCCCTGTGGTTCATTCGGA         1207           1005         GGAGGTTGCGGAAAAACCTTGATCATCGTCCTCGTCGTGGTTCATTCGGA         1064           0y         1208         CTGTGCTGGCCATCTCCTCGCCCTTTCATCGTCGTCGTCGTGGTTCATTCGGA         1064           0y         1208         CTGTGCTGGCCATCTCTCGCCCTTTCATCGGCGTCAAGTCATCGAGATCCAGTACG         1267           1065         CTGTGCTGGCCATCTCTCGCCCTTTCATCGAGGTCAAGATCCAGTACG         1124           0y         1268         TGCACAGCTTGGAACCTGGACATCATCCCTATGGAACACGAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCCAGACTTGGAACACGTCCAGACTCAGACCCAGACTTGGAACACGTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACGCCCAGACCCAGACCCCAGACTTGGAACACCAGACCCAGACCCAGACCCAGACCCCAGACTTGGAACACCCAGACCCAGACCCAGACCCCAGACCCCAGACCCCAGACCCCAGACCCCAGACCCCAGACCCCAGACCCAGACCCAGACCCAGACCCCAGACCCAGACCCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCACACACCCCAGACCACACACACCAC
2544 TCCAAATGCGGATCACTGGTCAGATGGACTCTAGAAGCACTGAGCTCCCTGTCTCTGGAA 2603 2541 TCCAAATGCGGATCACTGGTCAGATGGACTCTAGAAGCACTGAGCTCCCTGTCTCTGGAA 2603 2604 GTATTTAAGAAAAGGCTGGGCCGAGGCTGTCAGCAGCTTTGGG 2663 2604 GTATTTAAGAAAAGGCTGGGCCAGAGCTCTAGGCCTGTAATCCCAGACTTTGGG 2663 2604 GTATTTAAGAAAAGGCTGGGCAGAGGAGAGGCTGAGCCTGTAATCCCAGACTTTGGG 2663 2604 GTATTTAAGAAAAGGCTGGGCAGGAGGAGGCTGAGCCTGTAATCCCAGACTTTGGG 2660 2604 AGGCCGAGGCAGGCGAGGCAGGGCAGAGGGTTTGAGAACAGCCTGGCCAACATGGT 2723 2604 AGGCCGAGGCAGGCGGATCACCTGAGGTGAGGATTTGAGAACAGCCTGGCCAACATGGT 2720		2941 AGISAGGICGIGCCACIGCATICCAGGCAGGGAGGCAGGCTCTGTCTCA 2900 2904 AGAAAAAAAAA 2917 2901 AAAAAATAAAAA 2914	10-10 2 10-10 2 10-10 2 10-10 3-10 3-10 3-10 3-10 3-10 3-10 3-10	RAICH AFLIAGION NUMBER: RRICH FILING DATE: UNBER OF SEQ ID NOS: 4096 UNBER OF SEQ ID NOS: 2.1  COT DATE: UNC 997  LENGTH: 2759  TYPE: DAA  ORGANISM: Homo sapiens 0-104-047-997	Second Similarity   95.2%;   Pred. No. 0;   Second	

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	RESULT 3 US-10-104-047-986   Sequence 986, Application US/10104047   Patent No. 6943241   GENERAL INFORMATION:   APPLICANT: HELIX RESEARCH INSTITUTE   TITLE OF INVENTION: No. 6943241e1 full length cDNA   FILE REFERENCE: H1-A0105   CURRENT FALING DATE: 2002-03-25   CURRENT FALING DATE: 2002-03-25   PRIOR PILING DATE: 3 PRIOR FILING DATE: 3 PRIOR FILING DATE: 3 FRIOR FILING DATE: 4 FRIOR FILING DATE: 4 FRIOR FILING DATE: 4 FRIOR FILING DATE: 5 FRIO	Query Match         45.4%; Score 1325.8; DB 3; Length 2625;           Best Local Similarity         95.8%; Pred. No. 8.7e-314;           Matches 1338; Conservative 0; Mismatches 2; Indels 1; Gaps 1;           Oy         1562 CCCCAGATCTCATCCTGACTCCTAATCTTCCAAGGGTGCCAGCCCTCCG 1621           Db         1286 CTCCAGATCTCTGAACCCAGCTCTTTCAGCTGCTTCTACAGGGTGCCAGCCCTCCG 1345           Oy         1622 TTCATCTCTGAAACCCAGCATCCTTTCAGCTGCTTGAAAACATTGTATTTTTTTT
1388   CGGAGTTTGTGCTGCCCAGGTCTGAAGAGAGCCAGGTGGCACCAGTGGAAAACAGGT   1447	1868 TGCTTGTCACCCGCTCCAGGTTGGAGCCACAGACACCCACC	

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Sequence 3, Application US/09174937
Patent No. 6756212
GENERAL INFORMATION:
APPLICANT: Khoaddoust, Mehran
TITLE OF INVENTION: Isolated Proteins and Nucleic Acid Molecules Having
TITLE OF INVENTION: Homology to NIP2 Proteins and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/174,937
CURRENT FILING DATE: 1998-10-19
NUMBER OF SEQ ID NOS: 9
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38.1%; Score 1113; DB 3; L
Best Local Similarity 100.0%; Pred. No. 5.8e-262;
Matches 1113; Conservative 0; Mismatches 0;
        2605 GACAGAGCAAGACTCTGTCTC 2625
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SEQ ID NO 3
LENGTH: 1113
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; LOCATION: (1)..(1113)
US-09-174-937-3
                                                  RESULT 4
US-09-174-937-3
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                                                                                                                      1645 GGTCTGCGTCCTTTCCTTTCCCTCCAGAATGCGGCCTCAGACCTAGAAGCTCAA
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                                            TTCTCTTGCTTGTCACCCCCTCCAGGTTGGAGCCACAGACACCCCACCGCCACCCCGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----CCATGATCCCACCACAACAACATTCCTGCC 363
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                                                                                                                                                                                                                                                        Sequence 6, Application US/09174937

Patent No. 6756212
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Homology to NIP2 Proteins and Uses Thereof
FILE REFERENCE: mino61
CURRENT APPLICATION NUMBER: US/09/174,937
CURRENT FILING DATE: 1998-10-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 966
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                                                                                               CCTGGGCGACAGACACTCT 2897
                                                                                                                                        300 CCTGGGCGACAGAGCAAGACTCT 322
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ORGANISM: Homo sapiens
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; LOCATION: (1)..(966)
US-09-174-937-6
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US-09-621-976-14512

Sequence 14512, Application US/09621976

Factor No. 653063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

APPLICANT: Jobert, S.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm
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Pred. No. 4.8e-66;
3; Mismatches 0;
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Best Local Similarity 98.8°
Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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LENGTH: 322
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Sequence 12513, Application US/09949016

Sequence 12513, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PRILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSECES for Windows Version 4.0

SEQ ID NO 12513

LENGHENT 103987
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                                                                                                                                1000 ATCATGGAGAACCICITCCIGIACGICAICAGCAGCITAGAGCICCTGGIGGCIGAGGAC
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         829 CTGTGGCGGACAGTGATCATCGGGGAGCAAGAGCACCGTATAGACCTGCACATGATCCGG
                                                    443 CTTTGGATGACAGTGGTCATTGGAGAACAAGAGCAGCGCATTGACATGAAGGTCATCGAG
                                                                                                 989 CCTTACATGAAAGTGGTCACCCACGG-----AGGGTACTACGGCGAAGGCCTCAAC
                                                                                                                                                                                          940 GCCATCATCGTCTTCGCAGCCTGCTTCCAGACAGCAGCACCCCCCGACTACCACTAC
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                                                                                                                                                                                                                                                                                                                   623 GTCATGGAAAATCTTTTCCTATAAGTAATAAGTACTTTAGAGTTGATGGTAGCTGAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                        683 TATATGATTGTGTACTTGAATGGTGCAACCAAGAAGGAGGATGCCAGGGCTAGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  803 ATTGTTCATCCATCTTGGTTCATCAGACAATCCTTGCTGACACGACCTTTTATAAGT
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89.2%; Pred. No. 1.8e-48;
tive 0; Mismatches 32
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Best Local Similarity 89.2
Matches 272; Conservative
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                                                                                                                                                                                                                                                                                                                      1240 GTCAAGTTCATCAACAAGATCCAGTACGTGCACAGCTTGGAAGACCTGGAGCACTCATC 1299
                                                                                                                                                                                                                             ATCGTCCACCCCTCGTGGTTCATTCGGACTGTGCTGGCCATCTCTCGCCCTTTCATCAGC 1239
GTCATGGAAAATCTTTTCCTATATGTAATAAGTACTTTAGAGTTGATGGTAGCTGAAGAC 660
                                                                                                                                                                                                                                                                                                                                                                   841 TCAAAATTCAGCAGTAAAATTAAATATGTCAATAGCTTATCAGAACTCAGTGGGCTGATC 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGGCGTGCTGAGTCCCAGTGCTGCAGACATGAGGCCTGAACCTCCTAATTCTCTGGAT 178
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Sequence 4, Application US/09174937

Batent No. 6756212

GENERAL INFORMATION:

APPLICANT: Khodadoust, Mehran

TITLE OF INVENTION: Isolated Proteins and Nucleic Acid Molecules Having

TITLE OF INVENTION: Homology to NIP2 Proteins and Uses Thereof

FILE REPERRUCE: maio61

CURRENT APPLICATION NUMBER: US/09/174,937

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4
                                                                       721 ATGAAGAATGCTACCAGATGATTGACGGAGGATTTGAATTTGAATTCATC
                                                                                                                                                                                                                                                                      ATTGITCATCCATCITGGITCATCAGAACAATCCTTGCTGACACGACCTTTTAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 CTTAATGACACTCCACGGAGAATCAAGCTCACAGCCCCAAATATCAATCTTTCTCTG
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                                                                                                                                        CTGAAGAAGTGCTACCAGATGATCGACCGGAGGTTGCGGAAAAACCTGAAGTCCTTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529 ITCAACGGAGCGCAICGIAAGAAGAAGACGCIGGIGGCCCCCAGAGAICAACAITICICIG
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Pred. No. 9.3e-64;
0; Mismatches 283; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   CCTATGGAACACGTCCAGATCCCAGACTGCGTCCT 1334
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Best Local Similarity 62.5%;
Matches 547; Conservative
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; LOCATION: (23)..(988)
US-09-174-937-4
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Sequence 15793, Application US/09949016

Sequence 15793, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PLILNG DATE: 2000-10-20

PRIOR PLILNG DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOFTHARE FEBERGO FOR Windows Version 4.0

LENGTH: 33712
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Sequence 15091, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT PRILICATION NUMBER: US/09/949,016

CURRENT PLING DATE: 2000-04-14

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-00-08

NUMBER OF SEQ ID NOS: 207012

SOPTHARE: PSECSE FOR WINDOWS VERSION 4.0

SEQ ID NO 15091

LENGTH: 193169
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                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15793
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ORGANISM: Human
FEATURE:
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENITON: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENITON: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENITON: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENITON: WINDER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR PILING DATE: 2000-01-20
FRIOR PILING DATE: 2000-10-03
FRIOR PILING DATE: 2000-10-03
FRIOR PILING DATE: 2000-09-08
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                     47908 AAAGTCTGGGCTGGCGGGGGCTCATGCCTGTAATCCCAGCACTTTGGGTGGCTGAGG 47849
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                                                                                                                                                          2733 TCTCTACTAAAATACAAAATTAGCCAGGCGTGGTGGCAGGTGCCTGTAATCCCAGCTA 2792
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89.2%; Pred. No. 1.8e-48;
tive 0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                          Sequence 17050, Application US/09949016
Patent No. 6812339
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Best Local Similarity 89.23
Matches 272; Conservative
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US-09-949-016-17050
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LENGTH: 103988
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RESULT 10

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71006 CTCGTCTCTACTAAAATACAAAATTAGCCGGGCATGGTGGCATGCACCTGTAATCCCA 71065
                                                                                                                                                      71126 GCCGAGATGGCGCCCACTGCAGCCTGGGTGACAGAGGGAACTCCATCTCAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4703 AAGAGGGTTGAGGCCGGGGGGGGTGACCTGTAATCCCCAGCACTTTGGGAGGCCG
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                                                                                   71066 deractececadecercadecacadaarecerraaacercaaaceaagacerceacada
                                                                                                                       2491 TGTTCGGGAGGCAAATTTCCCTAGGAAAAAAAAAAACAGACTTTTCTAATGTGGCTCCAAAT
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Fatent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND FILE REFERENCE: CLO01307
CURRENT FILING DATE: 2000-04-14
FRICA PLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-00-10-20
FRIOR PLICATION NUMBER: 60/231,768
FRIOR FILING DATE: 2000-10-20
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR FILING DATE: 2000-09-08
FRIOR PELING DATE: 2000-09-08
FRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 13408
FRIOR FILING DATE: 49378
FRIOR FILING DATE: 49378
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                                                                                                                                                                                                                                      71186 AAAAAAAAA 71195
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Best Local Similarity 75.5°
Matches 324; Conservative
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ORGANISM: Human
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Patent No. 6812339

GENERAL INFORMATION: Craig et al.

GENERAL INFORMATION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLILNG DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHARD FESTER OF WINDOWS VERSION 4.0

SEQ ID NO 17521

LENGTH: 87734
                                                                                                                                                                                                76689 GAAGGAGAGACTTGCAGTGAGCCGAGATTGTGTGCTACTGCATTCCAGCGTGGGCGACAGAG 76630
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                                                                                                                                    0; Mismatches
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Pred. No. 3.7e-
0; Mismatches
                                                                                               Score 241.2;
Pred. No. 3.
; NAME/KEY: misc_feature
; LOCATION: (1)...(193169)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15091
                                                                                               85.2%;
                                                                                                                                  281; Conservative
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Best Local Similarity 88.1
Matches 273; Conservative
                                                                                                                 Similarity
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US-09-949-016-17521
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Best Local S
Matches 281
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FEATURE:
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                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERRACE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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Sequence 14964, Application US/09949016
Sequence 14964, Application US/09949016
Sequence 14964, Application US/09949016
Sequence 14964, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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8.2%; Score 239.6; DB 3;
Best Local Similarity 87.3%; Pred. No. 2.7e-48;
Matches 274; Conservative 0; Mismatches 39;
                                                                                                                Sequence 17290, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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4403 AAAAGAAAA 4395
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; ORGANISM: Human
US-09-949-016-17290
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LENGTH: 11929
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13006 GCCAAAATCGCACCACTGCACTCCAGCCTGGGCAAAGAAAACA 22947
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                                                                                                                                                                                                                                                                                                                                                                                              Length 24221;
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Pred. No. 4e-48;
0; Mismatches 36; Indels
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 14964
LENGTH: 24221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: March 5, 2006, 04:34:12
Job time : 506 secs
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.0%;
Matches 272; Conservative
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                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM nucleic - nucleic search, using sw model

March 5, 2006, 03:44:45 ; Search time 2058 Seconds (without alignments) 11724.998 Million cell updates/sec Run on:

US-10-699-941-3 2918

Title: Perfect score:

Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

9793542 seqs, 4134689005 residues Searched:

19587084 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	Sequence 3. Appli	œ	0	, ,	2 -	980		19	-				9	340		644	6819.		_	221	Sequence 28000. A		Sequence 152869,
		QI.	US-10-699-941-3	US-10-699-941-8	US-10-104-047-997	US-10-699-941-10	US-10-699-941-11	US-10-104-047-986	US-10-699-941-1	US-10-450-763-16127	US-09-918-995-2540	US-10-723-860-4072	US-10-756-149-4047	US-10-487-593-2	US-09-873-367C-644	US-09-968-007A-349	US-09-968-007A-729	US-10-843-641A-644	US-10-843-641A-6819	US-10-843-641A-7199	US-10-220-891-19	US-10-357-930-22138	US-10-357-930-28000	US-10-027-632-152869	US-10-027-632-152869
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		Score	2918	2916.4	2598.2	1438.2	1438.2	1325.8	854.6	675	420.4	330.4	330.4	327.6	318.2	318.2	318.2	318.2	318.2	318.2	315.8	302.2	302.2	267	267
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US-09-925-065A-515679	US-09-814-353-13015	US-10-034-650-34	US-10-741-601-5729	US-09-925-065A-594866	US-10-027-632-263139	US-10-027-632-263139	US-10-417-375-108	US-09-925-065A-594865	US-09-925-065A-55092	US-09-764-891-8024	US-09-925-065A-482665	US-09-925-065A-563212	US-10-027-632-251984	US-10-027-632-251984	US-10-741-601-5691	US-10-741-600-17762	US-09-925-065A-621024	US-09-925-065A-84578	US-10-322-281-456	US-10-087-192-664	US-09-925-065A-723891	
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243.6	243.6	241.8	241.6	241.4	240.6	240.6	240	239.8	239.6	239.6	239.5	239.2	239.2	239.5	239.2	239.2	239	239	239	238.8	238.6	
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## ALIGNMENTS

RESULT 1  US-10-699-941-3  Sequence 3, Application US/10699941  Publication No. US20040146900A1  GENERAL INFORMATION:  APPLICANT: Burmeister, Margit  TITLE OF INVENTION: Ataxia Associated Gene and Protein  FILE REFERENCE: UM-08441  CURRENT APPLICATION NUMBER: US/10/699,941  CURRENT FILING DATS: 2003-11-03  NUMBER OF SEQ ID NOS: 62  SOFTWARE: Patentin version 3.2  SEQ ID NO 3  LENGTH: 2918  TYPE: DNA  ORGANISM: Homo sapiens  US-10-699-941-3	Query Match 100.0%; Score 2918; DB 7; Length 2918; Best Local Similarity 100.0%; Pred. No. 0; Matches 2918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			121   CTGCACCCACCCACCCTGCACAAAAGACTGGGGGGGGCTGGCCACGTCGCCCTGGG 180	181 TGACCTTCCTCGATGCAGAATCCGCCCTGCGAGCATCCTTCCT
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57045 CCGCTGCCAACCATCCTTGTCCTCCGATTGCAAAATGACACCCCAGTAATCTAGAACATT
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                                                       2375 AGCAAGAGAAGATACAGGGTATCGGGCCTTTCAGTGTTTCAGAAGTCATTCGGGAAGAT
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                         1535 AGAAAACCTCTGTCAGACGCCCACTGGCCCCAGATCTCATCCTGCCTCATCCTGAGTCCC
           TGGGAGGCTGAGGCATGAGAATCACTTAAACCTGAGAGGCAGAGGTTACAGTGAGCCAAG
                                                             CTTGAAAACATTGTATTTTTTTTTTTAACGATGCAGTATTTGTGCGTTTCCAGAAAAGGG
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                          Sequence II, Application US/10699941
; Publication No. US20040146900A1
; GENERAL INFORMATION:
; APPLICANT: Burmeister, Margit
; TITLE OF INVENTION: Ataxia Associated Gene and
; FILE REPERENCE: UM-08441
; CURRENT APPLICATION NUMBER: US/10/699,941
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 59884
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NAME/KEY: misc feature

LOCATION: (49102)..(49201)

OTHER INFORMATION: n is a, c, FRATURE:

NAME/KEY: misc feature

LOCATION: (55664)..(5763)

US-10-699-941-11
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Best Local Similarity 99.8%;
Matches 1440; Conservative
                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                            AAA 45162
                                                                                                                   2915 AAA 2917
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US-10-699-941-11
           2795
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us-10-699-941-3.rnpbm

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             CTCCCCCAACCCAGCGTCAGGCTGGGACACGCCAACGCTGTTCCGGGTTGGAACAGCAGA 2064
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                                                                                                                             2125 CGTTTGAGTGTTTCAGAAGTCATTCGGGAAGATAAATCCAGTGCGCTGGCCGCAGCCACC
                                                             ACTGAGCTCCCTGTCTCTGGAAGTATTTAAGAAAAGGCTGGGCCAGGCACGATGGCTCAC
                                                                                                                                                                         TGCATTCAAAGCTTGGACCAGCGGGTTCTTGTTCGGGAGGCAAATTTTCCCTAGGAAAAAG
                                                                                                                                                                                                                                                         2245 AAGACAGACTITICTAATGTGGTCCAAATGCGGATCACTGGTCAGAGGCTCTAGAAGC
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                                                                                                           2402 CGTTTGAGTGTTTCAGAAGTCATTCGGGAAGATAAATCCAGTGCGCTGGCCGCAGCCACC
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TITLE OF INVENTION: Ataxia Associated Gene
FILE REFERENCE: UM-08441
CURRENT APPLICATION NUMBER: US/10/699,941
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.2
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Publication No. US20040146900A1
GENERAL INFORMATION:
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Best Local Similarity 75.0°
Matches 1153; Conservative
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US-10-699-941-1
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45.4%; Score 1325.8;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1338; Conservative 0; Mismatches
US-10-104-047-986
; Sequence 986, Application US/10104047
; Publication Wo. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; RUMRENT FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver: 2.1
; SEQ ID NO 986
; LENTH: 2625
                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-986
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CGAGA 1377
CGAGA 1377
CGAGA 1437
CGAGA 1437
CGAGA 1497
CGA 1554  645

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Sequence 4072, Application US/10723860
Publication No. US20040253606A1
Sequence 4072, Application US/10723860
Publication No. US20040253606A1
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Solutik, Albert
APPLICANT: Solutik, Albert
TITLE OF INVENTION: Methods for Biagnosis of Soft Tissue Sarcoma, Compositions FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
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184 ACGGGGGTGGAACTGCTTGGCAGCCCGGTGGAAGACACATCCTCCTCCTCCCAACACGCTA 243
                                                                                                                           AATGGCAACGAACTGGAGTGGGAAGACGACCCCCGTGGCCACCGCCAAGAACATGCCC 765
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                                                    244 AATTICAACGGAGGCGTCGTAAGAGGAAGACGCTGGTGGCCCCAGAGATCAACATTTCT
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SOFTWARE: Patentin version 3.2
SEQ ID NO 4072
LENGTH: 5656
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US-10-723-860-4072
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US-10-723-860-4072
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                             CAGCTCCCATGGGACCACCGAGCCACGCTCGGATGGAAAACGTGGACGTGAAGGAGG
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| Publication No. US20030073623A1
| GENERAL INFORMATION:
| APPLICANT: Hyseq. Inc.
| TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED |
| TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES |
| TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES |
| FILE REPERBENCE: 2011-756 |
| CURRENT PILING DATE: 2001-07-30 |
| PRIOR PILING DATE: 1999-01-20 |
| PRIOR FILING DATE: 1999-01-20 |
| NUMBER OF SEQ ID NOS: 38654 |
| SEQ ID NO 2540 |
| LENGTH: 485 |
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LOCATION: (1)...(485)
CTHER INFORMATION: n = A,T,C or
US-09-918-995-2540
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              649 ATTAACGTGGATGACATCGAGACCCCCGATGAGACCGACTCGCTGGAGTTCCTGGGGAAT
                                                                                                                         709 GGCAACGAACTGGAGTGGGAAGACGACCCCCGTGGCCACCGCCAAGAACATGCCCGGG
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Publication No. US20050064413A1
GENERAL INPORMATION:
APPLICANT: NACKGAWARA, AKTRA
APPLICANT: HATTORI, MASAHIRA
APPLICANT: HATTORI, MASAHIRA
APPLICANT: APATICANTON: NOVEL HUMAN BMCCI GENE
ILLE OF INVENTION: NOVEL HUMAN BMCCI GENE
FILE REFERENCE: 7388/80977
CURRENT PILICATION NUMBER: US/10/487,593
CURRENT PILING DATE: 2004-02-24
PRIOR APPLICATION NUMBER: PCT/JP02/08520
PRIOR PILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 55
SEQ ID NO 2
LENGTH 11690
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; ORGANISM: Homo sapiens
US-10-487-593-2
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                                GICTICGCAGCCIGCTICCTICCAGACAGCAGCCICCCCGACTACCACTACATGAG 1008
                                                                                                                                                                                                                                                        1957 GIGITTGCCGCCTGTTTTCTGCCAGACAGCAGTGGGGGGGGATTACCACTATGTCATGGAA 2016
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCTACAGGAGAGTCATTCTCACGGAGGATACTATGGGGACGGTCTAAATGCCATCATT 1956
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  CTGTGGCGGACAGTGATCATCGGGGGGGGCAAGAGCACGTATAGACCTGCACATGATCCGG
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Sequence 4047, Application US/10756149

PUBLICANT US20050181375A1

GENERAL INFORMATION:

APPLICANT: Aziz, Natasha

APPLICANT: Zlotnik, Albert

TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COI

TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC;

CURRENT APPLICATION NAMBER: US/10/756,149

CURRENT PILING DATE: 2004-01-12

NUMBER OF SEQ ID NOS: 5818

SOFTWARE PATENTIN VERSION 3.2
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Pred. No. 2.5e-84;
0; Mismatches 291; Indels 33;
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Best Local Similarity 63.3%;
Matches 558; Conservative
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US-10-756-149-4047
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APPLICANT: Endress, Gregory
APPLICANT: Augustus, Meena
APPLICANT: Endress (Reinhard
APPLICANT: Endress (Reinhard
APPLICANT: Endre Reinhard
APPLICANT: Carter, Keanhard
TITLE OF INVENTION: Signature Gene Sets
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
CURRENT APPLICATION NUMBER: U.S. 60/236,891
PRIOR APPLICATION NUMBER: U.S. 60/236,892
PRIOR PILING DATE: 2000-09-29
PRIOR PELING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-01
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SOUTHWARE: PATENTING DATE: 2000-11-01
SOUTHWARE OF SEQ ID NOS: 1067
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Pred. No. 8.7e-81;
0; Mismatches 288;
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Best Local Similarity 63.2%;
Matches 558; Conservative
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US-09-873-367C-644
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                                                                                                                                                                                                                                             7547 GAGGCGTGCTGAGTCCCAGTGCTGCAGACATGAGGCCTGAACCTCCTAATTCTCTGGAT
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                                             Length 11690;
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                                      Score 327.6; DB 9;
Pred. No. 2.2e-83;
0; Mismatches 289;
                                      Query Match
Best Local Similarity 63.2%;
Matches 557; Conservative
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Sequence 644, Application US/09873367C Publication No. US20030165839A1 GENERAL INFORMATION: Paul APPLICANT: Young, Paul APPLICANT: Soppet, Daniel

RESULT 13 US-09-873-367C-644

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TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Usining Signature of Invention: Gene Sets
TITLE OF INVENTION: Gene Sets
TITLE OF INVENTION: Gene Sets
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-71
CURRENT APPLICATION NUMBER: US/60/237,172
PRIOR APPLICATION NUMBER: US/60/237,173
PRIOR PLILNG DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 1001
SOFTWARE: PREAMER: PREAMER 
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Pred. No. 8.7e-81;
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Publication No. US20040115625A1

GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard

TITLE OF INVENTION: Gene Sets

TITLE OF INVENTION: Gene Sets

TITLE OF INVENTION: Gene Sets

FILE REFERENCE: 689290-71

CURRENT APPLICATION NUMBER: US/09/968,007A

CURRENT FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: US/60/237,172

PRIOR APPLICATION NUMBER: US/60/237,294

PRIOR FILING DATE: 2000-10-02

PRIOR FILING DATE: 2000-10-02

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-02

PRIOR PILING DATE: 2000-10-03

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                                                                                                                                                   CCCCTCGTGGTTCATTCGGACTGTGCTGGCCATCTCTCGCCCTTTCATCAGCGTCAAGTT
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                                                                           GGGGTGGAACTGCTTGGCAGCCCGGTGGAAGACACATCCTCCTCCCAACACGCTAAAT
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Pred. No. 8.7e-81;
0; Mismatches 288; Indels 37;
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Best Local Similarity 63.2%;
Matches 558; Conservative
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CORGANISM: Homo sapiens
US-09-968-007A-349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2014 AATCTTTCCTATATGTAAGTACTTTAGAGTTGATGGTAGCTGAAGACTATATGATT 2073
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                                  GGGGTGGAACTGCTTGGCAGCCCGGTGGAAGACACATCCTCCTCCTCCCAACACGCTAAAT
                                                                                                   TTCAACGGAGCGCATCGTAAGAGGAAGACGCTGGTGGCCCCCAGAGATCAACATTTCTCTG
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                                                                                                                                                                                                                                                                                                             709 GGCAACGAACTGGAGTGGGAAGACGACCCCCCTGGCCACCCCCAAGAACATGCCCGGG
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                                                               1510 GAGGGGTGCTGAGTGCTGCAGACATGAGGCCTGAACCTCCTAATTCTCTGGAT
37; Gaps
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Indels
0; Mismatches 288;
Conservative
Matches 558;
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Search completed: March 5, 2006, 05:22:00 Job time: 2067 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM nucleic - nucleic search, using sw model

March Run on:

5, 2006, 03:46:55 ; Search time 810 Seconds (without alignments) 7898.360 Million cell updates/sec

US-10-699-941-3 2918

Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

7218535 segs, 1096242582 residues Searched:

14437070 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Database :

/cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*/cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq3:\*/cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq4:\*/cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq4:\* prodata/1/pubpna/USO9\_NEW\_PUB.seq: prodata/1/pubpna/USO9\_NEW\_PUB.seq1 prodata/1/pubpna/USI0\_NEW\_PUB.seq: prodata/1/pubpna/USI0\_NEW\_PUB.seq: ptodata/1/pubpna/US11\_NEW\_PUB.seq /ptodata/1/pubpna/US08 /ptodata/1/pubpna/US06 /ptodata/1/pubpna/US07 ptodata/1/pubpna/PCT | ptodata/1/pubpna/US09 Applications NA New:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Regult		2					
Q	Score	Match	Match Length DB	DB	ΩI	Description	
-	2598.2	89.0	2759	6	US-11-072-512-997	Segmence 997.	Ann
~	1325.8	45.4	2625	σ	US-11-072-512-986		Ann
G + 3	243.6	8.3	623	9	US-09-925-065A-515679		0
4 , - 0	241.6	8.3	403278	8	US-10-995-561-13421		A
'n	241.4	8.3	260	9	US-09-925-065A-594866		
ς. Sy	240.8	8.3	138627	7	US-10-330-773-159		App
مبر	239.8	8.2	260	9	US-09-925-065A-594865		
80	239.6	8.2	628	9	US-09-925-065A-55092		A
σ	239.2	8.2	562	9	US-09-925-065A-482665	Segnence 482665.	
10	239.2	8.2	611.	9	US-09-925-065A-563212	Sequence 563212	2
11	239.2	. 8.2	67126.	8	US-10-995-561-13342	Semience 13342	4
12	239.2	8.2	127340	12	US-11-112-908-35	Semence 35 Ann	App
13	239	8.2	483	9	US-09-925-065A-621024	Sequence 621024	14
c 14	239	8.2	1082	9	US-09-925-065A-84578	Seguence 84578	A
c 15	238.6	8.2	2649	9	US-09-925-065A-723891	Sequence 723891	1.
3 16	238.4	8.2	547	ø	US-09-925-065A-657480	Segmence 657480	
c 17	238.4	8.5	623	9	US-09-925-065A-687639		
Ċ 18	238.4	8.2	623	9	US-09-925-065A-687640		
13	238.2	8.2	624	9	US-09-925-065A-849333		3
20	238	8.2	180531	σ	115-11-114-798-57	5	

Sequence 75055. A	692997.			Seguence 624539.				486749		Sequence 83. Appl	37303	Sequence 94635. A	Sequence 92083. A	Sequence 696162,	Sequence 105, App	Sequence 106, App	10, A	Seguence 94636. A	Sequence 1355. Ap	_:	Sequence 9. Appli	Sequence 443115.	Sequence 930747.	
6 US-09-925-065A-75055	6 US-09-925-065A-692997	6 US-09-925-065A-563211	6 US-09-925-065A-624538	6 US-09-925-065A-624539	6 US-09-925-065A-197384	6 US-09-925-065A-337721	6 US-09-925-065A-8768	6 US-09-925-065A-486749	6 US-09-925-065A-8769	12 US-11-121-086-83	6 US-09-925-065A-873038	6 US-09-925-065A-94635	6 US-09-925-065A-92083	6 US-09-925-065A-696162	12 US-11-121-086-105	12 US-11-121-086-106	12 US-11-121-086-10	6 US-09-925-065A-94636	9 US-11-072-512-1355	8 US-10-995-561-13512	12 US-11-121-086-9	6 US-09-925-065A-443115	6 US-09-925-065A-930747	6 US-09-925-065A-282862
694	1288	611	482	482	570	621	883	682	883	187745	009	661	1980	1980	171486	179777	199321	661	3125	40000	196200	574	553	280
8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1
237.8	237.8	237.6	237.4	237.4	237.4	237.2	236.6	236.2	236.2	236.2	236	236	236	236	236	236	235.8	235.6	235.6	235.6	235.4	235.2	235	235.
21	22	23	24	25	56	27	28	53	30	31	32	33	.34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

RESULT 1

		ENERAL INFORMATION: APPLICANT: ISOGAI, TAKAO	SUGIYAN		: WAKAMA	: SATO, H	APPLICANT: ISHII, SHIZOKO	APPLICANT: ISONO, YUTKO	: HIO, YI					: SEKI, NAOHI				CANT: MASUHO, YASUHI	н	FERENCE: 084335-0191	APPLICATION NU	FILING DATE: 2005-03-07	TOR PILING DATE: 2007350,978	APPLICATION NUMBER:	FILING DATE: 2001-11-05	MBER OF SEQ ID NOS: 4096	FTWARE: PatentIn Ver	O ID NO 997	ă	ORGANISM: Homo sapiens	/66-216-2/O-
US-11-072-	, Publica	APPLIC	, APPLIC	; APPLIC	; APPLIC	, APPLIC	; APPLIC	APPLIC	, APPLIC	; APPLIC	, APPLIC	, APPLIC	, APPLIC	, APPLIC	, APPLIC	, APPLIC	, APPLIC	, APPLIC	; TITLE (	; FILE R	; CURRENT	Z	PRIOR			, NUMBER	; SOFTWA	SEQ ID	TYPE:	; ORGAN:	7/0-77-50

Gaps Query Match

89.0%; Score 2598.2; DB 9; Length 2759;
Best Local Similarity 95.2%; Pred. No. 7.5e-25;
Matches 2756; Conservative 0; Mismatches 3; Indels 136;

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1945 GCCACCGGGCAAACCCCGTCAATACCTCCCACCAAGGAATGAGAATGTGGACCTCACTG 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1405 AACGATGCAGTATTTGTGCGTTCCAGAAAGGGCCCAGCTCTGAGCCCCTCACCCTTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1802 GTGGCCTCCGCTCCTGCCAGCCCCTGTGGTCAGAGCTGGATACAAGATTCAAGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1765 CACACCCATGGTTTTTCATTTGACCCGCCCCTTCTCGCTCATAATGACACCCCAGCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1825 TTGAGAGGATCAGAGCCCATTGCACAAGAAGAGCCGCTGCCAACCATCCTTGTCCTCCGA
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                 Query Match
45.4%; Score 1325.8; DB 9; Length 2625;
Best Local Similarity 99.8%; Pred. No. 5.1e-10;
Matches 1338; Conservative 0; Mismatches 2; Indels 1;
 APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084325-0131
CURRENT PELLORION NUMBER: US/11/072,512
CURRENT PELLING DATE: 2005-03-07
FRIOR APPLICATION NUMBER: US 60/350,978
FRIOR PILING DATE: 2002-01-25
FRIOR APPLICATION NUMBER: US 5001-379298
FRIOR PILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 986
LENGTH: 2625
                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiene
US-11-072-512-986
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        AATCCCAGACTTTGGGAAGCCCAAGGCAGCGGATCACCTGAGGTGAGGTTTGAGAACA
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        AATCCCAGAGCCTAGGGCAGGCGGATCACCTGAGGTGAGGAGTTTGAGAACA
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                                                                                                                                      GACTITICTAATGTGGTCCAAATGCGGATCACTGGTCAAAGGACTCTAGAAGCACTGAG 2587
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AATGACACCCCAGTAATCTAGAACATTCTCAAGCCCCTTTAACTCAGATGTCAAGCCACC 2084
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                                                           GAAACTGGCTCTGAAATAGGCAGACCTAGCAAGAGGAAGATACAGGGTATCGGCGCTTTG
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                                     GGGCAAACCCCGTCAATACCTCCCAAGGAATGAGATATGTGGACCTCACTGCTCCCC
                                                                                                                 CAACCCAGCGTCAGGCTGGACACGCCAACGCTGTTCCGGGTTGGAACAGCAGAGGCTCA
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Publication No. US20060029945a1
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: TSANO, TUN-ICHI
APPLICANT: TSANO, TUN-ICHI
APPLICANT: TSONO, TUNCO
APPLICANT: TSONO, TUNCO
APPLICANT: NAGANI
APPLICANT: NAGAI, KEIICHI
APPLICANT: NAGAI, KEIICHI
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SOSHIKWA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: SOSHIKWA, TSUTOMU
APPLICANT: NAGAHARI, KENJI
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; NAME/KEY: misc_feature
}; LOCATION: (1)...(403278)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13421
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERSNCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 13421
                                                                                                                                              185 CGAGGCGGGCAGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAA
                                                                                                                                                                                                                                                                                                                         265 AACCACTTGGGAAGCTGAGGCAGGATAATTGCTTAAACCCGGGAGGTGGAGGTTACAGTG
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                             2609 TAAGAAAAGCCTCGCCCAGGCACGATGGCTCACGCCTGTAATCCCAG-ACTTTGGGAGGC
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90.0%; Pred. No. 34;
tive 0; Mismatches
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Best Local Similarity 90.01
Matches 270; Conservative
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145 AAAAAAAA 136
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ORGANISM: Homo sapiens
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US-10-995-561-13421/c
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                    GGCTCAGAAACTGGCTCTGAAATAGGCAGACCTAGCAAGAAGAAGATACAGGGTATCGGG
                                                                                                                   CGTTTGAGTGTTTCAGAAGTCATTCGGGAAGATAAAATCCAGTGCGTGGCCGCAGCCACC
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GGCTCAGAAACTGGCTCTGAAATAGGCAGACCTAGCAAGAGGAAGATACAGGGTATCGGG
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US-09-925-065A-515679/C
i Sequence 515679, Application US/09925065A
; Sequence 515679, Application US/09925065A
; Sequence 515679, Application No. US20040181048A1
; GENERAL INFORMATION:
    APPLICANTY WANG, US-0040181048A1
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: NUMBER: US/09/925, 065A
; CURRENT APPLICATION NUMBER: US 60/243,096
; PRIOR APPLICATION NUMBER: US 60/244;
; PRIOR PILING DATE: 2000-11-20
; PRIOR PILING DATE: 2000-11-20
; PRIOR PILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR PILING DATE: 2001-01-16
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Publication No. US20040181048A1
GENERAL INFORMATION:
JENERAL INFORMATION:
JETLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: NUCLECTION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957068
SOFTWARE: FRASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                            Length 138627;
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                                                                                                                                                                                                                                                                                                                         Score 240.8; Di
Pred. No. 83;
0; Mismatches
                                                                                                                                                                                  // LOCATION: (1) ... (138627)
// OTHER INFORMATION: n = A,T,C or
US-10-330-773-159
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 89.1%;
Matches 271; Conservative
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Best Local Similarity 84.8%;
Matches 279; Conservative
                                                                                                                     FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(138627
                                                            TYPE: DNA ORGANISM: Homo sapiens
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US-09-925-065A-594865
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SEQ ID NO 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Mucleotide Polymorphisms in the Human Genome
FILE REPERBNCE: 108827, 135
CURRENT FILING DATE: 2000-108-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-10-66
PRIOR PILING DATE: 2001-10-66
PRIOR PILING DATE: 2001-01-66
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Pred. No. 7.6e+03;
1; Mismatches 47
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SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                               Sequence 594866, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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Publication No. US20060040262A1
GENERAL INFORMATION:
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Best Local Similarity 85.1;
Matches 280; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-925-065A-594866
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LANGTH: 560
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                                                                339 CAGCTACTTGGGAAGCTGAGGCAAGAGAATCACTTGAACCCGGAGGCAGGGTTGCAGT 398
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                                                                                                                                                                                                                                                                                                              Sequence 482665, Application US/09925065A

Publication No. US20040181048A1

GENERAL INPORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Sin;

TITLE OF INVENTION: Nuclectide Polymorphisms in the IPLE REFERENCE: 108027.135

CURRENT APPLICATION NUMBER: US/09/925,065A

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR PPLING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR PLING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16
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Pred. No. 8.1e+03;
0; Mismatches 38;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
                                                                                                                        2904 AAAAAAAAAAAA 2917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

8.2%;
Best Local Similarity 87.5%;
Matches 273; Conservative
                                                                                                                                                                                367 AAAAAAAAAAAA 380
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US-09-925-065A-482665
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US-09-925-065A-563212/c
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LENGTH: 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 GGAGGTGGATGTTTCARTGAGCCAAGATCGTGCCACTGCACTCCAGCCTGGGCGACAGAG 300
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2650 TCCCAG-ACTITGGGAGGCCGAGGCGGATCACCTGAGGTGAGGAGTTTGAGAACAG
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Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE:

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT PILING DATE: 2000-10-08

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRI
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Best Local Similarity 87.3%;
Matches 274; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS (
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERRNCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11342
LENGTH: 67126
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TLE OF INVENTION: Identification and Mapping of Single TILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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Pred. No. 7.5e+03;
1; Mismatches 29
                                                       TILE REPERRNCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-11-30
PRIOR PILING DATE: 2001-01-16
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Publication No. US20050272054A1
GENERAL INFORMATION:
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Best Local Similarity 89.6
Matches 267; Conservative
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; ORGANISM: Homo sapiens
US-10-995-561-13342
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US-09-925-065A-563212
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US-10-995-561-13342/c
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2783 ATCCCAGCTACTTGGGAGGCTGAGGCATGAGAATCACTTAAACCTGAGAGGCAGAGGTTA
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                                                                                                                     2723 TGAAACCTCATCTCTACTAAAATACAAAATTAGCCAGGCGTGGTGGCAGGTGCCTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 35, Application US/11112908
Publication No. US20050260659A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLA OF INVENTION: Exeast Cancer Biomarkers
FILE REPRENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT APPLICATION NUMBER: US 60/564,758
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR PILING DATE: 2004-04-23
PRIOR PILING DATE: 2004-04-13
PRIOR PILING DATE: 2004-11-30
PRIOR PILING DATE: 2004-11-30
PRIOR PILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR PILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/631,826
PRIOR PILING DATE: 2004-11-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: PatentIn version 3.3
SEQ ID NO 35
LENGTH: 127340
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87.5%; Pred. No. 92;
tive 0; Mismatches
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Matches 273; Conservative
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US-11-112-908-35/c
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CTGAGGCATGAGAATCACTTAAACCTGAGAGGCAGAGGTTACAGTGAGCCAAGATCGTGC 2861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 GECCAGGCGCGCGCGCTCAMGTCTGTAATCCCAGCACTTGGGAGGCCCAAGGTGGGTGGAT 353
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                                                                                                                                                                                                                                                                                                                                                                                          36; Indels
                                                                                                                                                                                                                                                                                                                                                      Score 239; DB 6;
Pred. No. 4.7e+03;
1; Mismatches 36;
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
FRIOR PELICATION NUMBER: US 60/243,096
FRIOR PELICATION NUMBER: US 60/243,096
FRIOR PELICATION NUMBER: US 60/25,147
FRIOR PELICATION NUMBER: US 60/25,147
FRIOR PELICATION NUMBER: US 60/250,092
FRIOR FLING DATE: 2000-11-30
FRIOR PELICATION NUMBER: US 60/261,766
FRIOR PELICATION NUMBER: US 60/289,846
FRIOR FILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 87.5%;
Matches 260; Conservative 1
                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-84578
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US-09-925-065A-723891/c
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LENGTH: 2649
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 124909 GAGCCAAGATCATGCCACTGCAGTCCAGCCTGGGCAACAGAGTGAGACTCCATCTTAAAA 124850
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US-09-925-065A-84578/c
Sequence 84578, Application US/09925065A
SETALL ON ON. US20040181048A1
SETALL INFORMATION:
APPLICANT Wang, David G.
TITLE OF INVENTION: Indentification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.2%; Score 239; DB 6; Best Local Similarity 89.0%; Pred. No. 9.2e+03; Matches 268; Conservative 1; Mismatches 31;
                                                                                                                                  US-09-925-065A-621024/c
; Sequence 621024, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
                                                                    124849 AAAAAAAAAAA 124838
                                  2907 AAAAAAAAAA 2918
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CRGANISM: Homo sapiens
US-09-925-065A-621024
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LENGTH: 483
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us.-10-699-941-3.rnpbn

US-09-925-065A-723891

Length 2649; Score 238.6; DB 6; Length Pred. No. 2.3e+03; 0; Mismatches 34; Indels Query Match
Best Local Similarity 88.5%;
Matches 270; Conservative (

2615 AAGGTTGGGCCAGGCACGATGGCTCACGCCTGTAATCCCAG-ACTTTGGGAGGCCGAGGC Gaps 1;

TTGGGAGGCTGAGGCATGAGAATCACTTAAACCTGAGAGGCAGAGGTTACAGTGAGCCAA 2853 2794

Search completed: March 5, 2006, 07:06:18 Job time : 815 secs

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OM nucleic - nucleic search,

Run on:

Title: Perfect score: Sequence:

Scoring table:

Searched:

		23	570.6	19.6	598	7	CR536713	
Gencore version 5.1.7		24	565.6	19.4	909	н	AW961890	
Copyrignc (c) 1993 - 2006 Biocceleration Ltd.		22	544.8	18.7	1022		BF530295	
		56	544	18.6	1043	~	BG913501	
		27	539	18.5	577	œ	DR002579	
uccieic search, using sw model		28	538.2	18.4	689	m	BQ179996	
		53	525.8	18.0	946	~	BF527108	
march 5, 2006, 03:31:06; Search time 11150 Seconds		30	520.6	17.8	548	7	CR773543	
(Without alignments)		31	502.6	17.2	673	_	CN219420	
12244.368 Million cell updates/sec		32	496.8	17.0	729	g	CA750371	
		33	483.4	16.6	509	7	CR628631	
30-10-699-941-3	บ	34	482.6	16.5	494	m	BQ312270	
		32	481.8	16.5	637	m	BQ044387	
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TOTAL THE TANK THE THE TANK TH		37	441.4	15.1	1471	<b>6</b> 0	DN717620	
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capop 10.0, capext 1.0		39	422.4	14.5	576	7	CN420200	

CR857898 3253 bp mRNA linear HTC 17-APR-2005 PONGO DYGMACUS MRNA; CDNA DKFZp459H1854 (from clone DKFZp459H1854). CR857898 GR857898 GR85786976 HTC. PONGO DYGMACUS (orangutan)	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Pongo.  1 (bases 1 to 3253)  1 (bases 2 to 3253)  2 (bases 3 to 3253)  2 (bases 4	Neuherberg, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKZ2), Email s.wiemannedkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the	Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp459H1854) is available at the RZPD Deutsches Resiourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.ed/cgi-bin/products/cl.ogi?CloneID=DKFZp459H1854 btrther information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.	Location/Qualifiers 1. 1353 1. 1353 1. 1253 1. 1253 1. 1353 1.	/dev_strate_stant + Sills + Calls   /dev_strate_stant   /dev_strat
CRESTL 1 CREST898 LOCUS CREST898 LOCUS DEFINITION PONGO PYGMAGUS ACCESSION CREST898 VERSION CREST898.1 GI KEYWORDS HTC. SOURCE PONGO PYGMAGUS ORGANISM PONGO PYGMAGUS			•	PEATURES Bource	gene
	1 by chance to have a the result being printed, re distribution.	Description		DQ05110B Pan trog1 CN420201 338775518 BG912726 602807930 CV0249652 251.2 Full DR002011 TC12.0419 BG913524 602811270 CN420203 1700066011 BU521943 AGENCOURT	
ST:*	8: gb_gest;* 9: gb_gest:* 10: gb_gest:* 11: gb_gest:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printe and is derived by analysis of the total score distribution.	SU Length DB ID	2553 4 C 21062 11 2104 4 A 2601 4 A 2603 4 A 3679 4 A 2603 4 A 2603 4 A	956 11 DQ023108 748 7 CN420201 865 2 BG912726 714 8 DR022011 876 2 BG913524 650 1 AL18250 639 7 CN420203	688 7 CR790459 630 6 CR153985 842 2 BF345891 609 2 BG310297 800 6 CA315557 609 2 BG819886
Database : EST:*  1: 9b 2: 9b 3: 9b 4: 9b 5: 9b 6: 9b	8: 9 9: 6 10: 11: Pred. No. is the score greater to and is derived	Result Query No. Score Match	1 2782.6 95.4 2 940 32.2 3 857.8 29.4 4 857.8 29.4 5 857.8 29.4 6 857.8 29.4 7 7 793 26.5	696.4 696.4 693.4 653 653 633.4	. 17 632.4 21.7 18 618 21.2 19 595.6 20.4 20 585 20.0 21 578.6 19.8 22 575.4 19.7

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			483.4	4.	16.	9	509		_	CR628631		CR628631	8631	DKFZp459L	
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			459	23	15.7	7	608			BF527542		BF527542	7542	602040445	
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										ALIGNMENTS	NTS				
•	RESULT CR8578	RESULT 1 CR857898													
	LOCUS	SC	_	CR857898	7898		•			3253 bp	MRNA	linear	TH	17-ADP-2005	'n.
	DBF	DEFINITION	_	Ponge	á	qmae	m ena	RNA		Pongo pygmaeus mRNA; cDNA DKFZp459H1854	459H1854	(from clone	DKPZ	DKFZn459H1854)	3 -
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	SOURCE	URCE ORGANISM		Pongo pygmaeus Pongo pygmaeus		pygmaeus pygmaeus		ora.	ng D	(orangutan)					
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				Homir	nida	e;	Hominidae; Pongo			1					
	REF	REFERENCE		1	(bases 1	18	to 3253)	253	_						
	Ā	AUTHORS		Koehrer, K.,	cer,	χ.	Beyer, A.,	r,A		Mewes, H.W	., Weil, B.,	Amid, C.,	Ogan	Osanger.A.	
				Fobo, G., Han, M.		Han		and		n, S.					
	ŏΊ	CONSRIM	-	The German cDNA	Serm	anc		g	Bor	Consortium					
	H	TITLE		Direct	it S	튭	Submission	G							
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			14	Зеве	arch	Ser	ter	9	PZ)		.wiemann@	s.wiemann@dkfz-heidelberg.de;	berg.	de;	
			w	3eque	ance	ρ g	BMF	= 2	Bio	sequenced by BMFZ (Biomedical Re	Research Center at	enter at the	•		
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Total number of hits satisfying chosen parameters:

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                                          GTGATCATCGGGGAGCAAGAGCACCGTATAGACCTGCACATGATCCGGCCTTACATGAAA
                                                                                                          GTGGTCACCCACGGAGGATACTATGGCGAAGGCCTCAATGCCATCATCGTCTTCGCAGCC
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ISSLELLVAEDWHIVYLNGATPRRRMPGISWIKKCTQMIDRRIRKNIKGLIIVHESWF
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Best Local Similarity 97.4%;
Matches 2840; Conservative
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121 TCCCTGCTGCTGATGACTTCTTGGATACCCCTGATGACCTGATGACTGAC	REF		REF		RAN G			AR L	REF	T SEE	<b>4</b>						OD COM		PEA	
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      GCGCGGATCTATTTGGGGACGGCACGGAGGACGGCAGCGCCCCCAACGGGCGCCTGT
                                                                    GGCGGACAGTGATCATCGGGGAGCAAGAGCACCGTATAGACCTGCACATGATCCGGCCTT
                                                                                                                                                           ACATGAAGGTGGTCACCCATGGAGGATACTACGGGGAAGGTCTCAACGCCATCATCGTGT
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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                                                          /note="unnamed protein product; putative
weakly similar to BCL2/ADENOVIRUS R1B 19-KDA
PROTEIN-INTERACTING PROTEIN 2 [Mus musculus]
(SWISSPROT 054940, evidence: PASTY, 52.5%ID, 94.7%length,
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                enriched mouse cDNA
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Pred. No. 3.9e-121;
0; Mismatches 337;
               full-length
tissue type="hypothalamus"
clone Tib="RIKEN full-lend
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                            dev_stage="adult"
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ilarity 75.1%;
Conservative
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EQEHR.DLHMIR.PYMKVVTHGGYYGEGLIAIIYPAACFLPDSSSPDYHYIMENIELIYV
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IRTVLAISRPFISWFFISKIQYYHSLBELERIIPMENIYOLPDCVLQYEEGRLRAKRES
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               CDNA library
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                                                                                                                     /note="unnamed protein product; putative
weakly similar to BCL2/ADENOVIRUS BIB 19-KDA
PROTEIN-INTERACTING PROTEIN 2 [Mus musculus]
(SWISSPROT|054940, evidence: PASTY, 52.5$ID, 94.7$length,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs

Adachi, 770 full-length CDNAs

S dacchi, 7. Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramcto, K., Hiramco, K., Haraka, T., Katoh, H., Kawai, J., Kojima, Y., Kodo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kodo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Salto, R., Saltoh, H., Sakai, K., Sakazume, N., Nakamura, M., Nishi, K., Nomura, K., Shinagawa, A., Shiraki, T., Sanc, H., Sanch, H., Sakai, C., Sakai, K., Sakazume, N., Sanc, H., Sanch, H., Sanch, H., Sakai, K., Sakazume, N., Sanc, H., Sanch, H., Sakai, K., Sakazume, N., Sanch, H., Sasaki, K., Sakazume, N., Sanch, H., Sasaki, K., Sakazume, N., Sanc, H., Sanch, H., Sakai, K., Sakazume, N., Sanch, H., Sanch, H., Sakai, K., Sakazume, N., Sanc, H., Sanch, H., Sakai, K., Sakazume, N., Sanch, H., Sakai, K., Sakazume, N., Sanch, H., Sanch, S., Sanch, S
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Nature 409, 685-690 (2001)
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                                   Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
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/drain="C57BL/63"
/db_xref="FANTOM_DB:3322401A10"
/db_xref="taxon:10090"
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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/tissue_type="head"
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The Analysis of the mouse transcriptome based on functional annotation of Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Nature 420, 563-573 (2002)

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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Rutuno,M., Haramgakkl.T., Haraka,A., Hashizume,W., Hayashida,K., Hayashida,K., Hayashida,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Katoh,H., Kawai,J., Kojima,Y., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasitoh,H., Sakai,C., Sakai,K., Sakazume,N., Salobeta,K., Shihagawa,A., Shiraki,T., Sogabe,Y., Tanaka,T., Tagawa,A., Takahashi,P., Takaku-Akahira,S., Muranaka,T., Tomaka,T., Towar, T., Yasunishi,A., Muranaka,Y., Tanaka,T., Towar, T., Yasunishi,A., Muranaka,M., Alakashizaki,Y., Tanaka,Y., Tanaka,Y., Towar, S., Taya,T., Yasunishi,A., Muranaka,M., Salob, S., Taya,T., Yasunishi,A., Muranaka,M., Tayaka,Y., Towar, S., Taya,T., Yasunishi,A., Muranaka,M., Salob, S., Taya,T., Yasunishi,A., Muranaka,M., Salob, S., Taya,T., Yasunishi,A., Muranaka,M., Tayaka,T., Towar, S., Taya,T., Toya,T., Taya,T., Taya,T.,
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Functional annotation of a full-length mouse cDNA collection
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         cloning
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/db_xref="taxon:10090"
    High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched library, clone.A330040009 product:weakly similar to BCL2/ADENOVIRUS BIB 19-KDA PROTEIN-INTERACTING PROTEIN 2 [Mus musculus], full insert sequence.
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Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230081007 product:weakly similar to BCL2/ADENOVIRUS E1B 19-KDA PROTEIN-INTERACTING PROTEIN 2 [Mus musculus], full insert sequence.

AK038990.1 GI:26332954

HTC; CAP trapper.

Mus musculus (house mouse)

SM Mus musculus (house mouse)

SM Mus musculus (bordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Mus.
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GTGCGGACCTGTTTGGGGACGGCTCTGCGGAAGACGGCAGTGCGGCCAACGGTCGTCTGT
                                                                            ACATGAAAGTGGTCACCCACGGAGGGTACTACGGCGAAGGCCTCAACGCCATCATCGTCT
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High-efficiency full-length cDNA cloning
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ISSLELLVAEDYMIVYLNGGYYGEGLANAIVFAACFLPSSSPDYTYIMENLFLYV
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IRTVLAISRPPISVKFISKIQYVHSLEELERLIPMENVOLPDCVLQYEEGRLRAAKRES
TRPPQPEFLLPRSSEKPETVEEEDRAARATEDQETSNS"
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                                     /note="unnamed protein product; putative
weakly similar to BCL2/ADENOVIRUS E1B 19-KDA
PROTEIN-INTERACTING PROTEIN 2 [Mus musculus]
(SWISSPROT|054940, evidence: FASTY, 52.5%ID, 94.7%length,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGCTGCGATGGCAGGGGAAACAGTGACTAAAGGGGGGACAGGGGTGCTGCTACTAACCCA
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Pred. No. 3.7e-121;
0; Mismatches 337;
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Matches 1155; Conserv
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                                                                                                                                                                                                                                                          ETDSLEFLGNGNELEWEDDT PVATAKNMPGDSADL FGDGSAEDGSAANGRLWRTVIIG
                                                                                                                                                                                                                                                                             EQEHRIDLHWIRPYMKVVTHGGYYGEGLMAIIVFAACPLPDSSSPDYHYIMENLFLYV
ISSLELLVAEDYMIVYLAGATPRRRMPGIGWLKKCYHMIDRRLRKNLKSLIIVHPSWF
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weakly similar to BCL2/ADEMOVIRUS BIB 19-KDA
PROTEIN-INTERACTING PROTEIN 2 [Mus musculus]
(SWISSPROT|054940, evidence: PASTY, 52.5*ID, 94.7*length,
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3679
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/codon start=1
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                    Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishil, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayahizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Please visit our web site for further details.
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs

Lister 420, 563-573 (2002)

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Sadachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Katoh, H., Kawai, J., Kojima, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kasuka, M., Ohsato, N., Nakanura, M., Nishi, K., Nomura, K., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakazume, N., Sasaki, D., Shibata, K., Shihagawa, A., Shizaki, T., Sogabe, Y., Taqami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission
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           Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
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AKO86723

Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930047M05 product; weakly similar to BCL2/ADENOVIRUS ELB 19-KDA PROTEIN-INTERACTING PROTEIN 2 [Mus musculus], full AKO86723

AKO86723.1 GI:26103717

HTC, CAP trapper.

Mus musculus (house mouse)

Scharyota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Buteleostomi; Sciurognathi; Muridae; Musinae; Mus.
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996 bp DNA linear GSS 02-JUN-2005 gene, VIRTUAL TRANSCRIPT, partial sequence,
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1 (bases 1 to 966)

Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Pledel-Alon, A., Tanenbaun, D.M., Civello, D., White, T.J., Nainsky, J., Aams, M.D. and Cargill, M. & Scan for Positively Selected Genes in the Genomes of Humans and
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                                                                                                                                           1081 GTATCTGAACGGCCCACGCCCCGGAGGATGCCTGGCATGGTTGGCTTGGCTGAAGAAGTG
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                       961 GTTTGCAGCCTGCTTCCTGCCAGATAGCAGCTCCCCAGACTATCACTACATCATGAGAA
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(er) PLoS Biol. 3 (6), R170 (2005)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
[dev stage="15 days embryo"
1. 2148
[note="weakly similar to BCL2/ADENOVIRUS R1B 19-KDA
FOTER.N-INTERACTING PROTEIN 2 [Mus musculus]
(SWISSPROT] [054940, evidence: PASTY, 52.5% ID, 94.7% length, match=972)"
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Pred. No. 4.7e-117;
0; Mismatches 340; Indels 4
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Best Local Similarity 74.9%;
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us-10-699-941-3.rst

	REBULT 9 CW420201 CW42020201 CW420201 C	Oy 217 ATCCTCTTCCTCTAGGCTCTGAAGGCCCGGGGAGCGTGGCCAGCTGCCCG 276
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.  PEATURES  Location/Qualifiers  Lorganism="Pen troglodytes" /mol_type="genomic DNA" /db_xref="taxon:9598" /locus_tag="HC13650"	Deat Local Similarity	781 INNINININININININININININININININININI

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LOCUS CV024962 699 bp mRNA linear EST 20-AUG-2004
DEFINITION 2512 Full Length CDNA from the Mammalian Gene Collection Homo
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/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI_CGAP_Brn67".
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
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                                                                                                                                                                                                   9
                                                                                                                                                         Length 865;
                                                                                                                                                     tch
25.0%; Score 730; DB 2; L
al Similarity 95.7%; Pred. No. 1.5e-101;
804; Conservative 0; Mismatches 30;
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602807930F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4940286
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Contact: Robert Strausberg, Ph.D. Email: Grapba-r@mail.nih.gov.
Contact: Robert Strausberg, Ph.D. Email: Grapba-r@mail.nih.gov.
Contact: Mobert Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.k.column: 07
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xxfe="taxon:9606"
/clone="IMAGE:4940286"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss"
                                                                                                                                                                       CGGATGGAAAACGTGGACGTGAAGGAGGAATGGCAGGACGAAGATCTTCCCAGGCCACTC
                                                                                                                                                                                                                                                AACATTTCTCTGGATCAGAGTGAGGGTCCCTGCTGTCCGATGACTTCTTGGATACCCCT
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                                 GGCAGGGCTCGCCTTTGTTTGCCAGTAAGGAGGAGGCTGTCTCAGCTGCAGAGGGGTC
                                                                     ATCCCTGCTTCAAGCCAGTGCCTCTTCCCAGCTCCCATGGGGACCACCGAAGCCACGCTC
                                                                                                                                               CGGATGGAAAACGTGGACGTGAAGGAGGAATGGCAGGACGAAGATCTTCCCAGGCCACTC
                                                                                                                                                                                                                           CCAGAAGAGACGGGGTGGAACTGCTTGGCAGCCCGGTGGAAGACACATCCTCCTCCTCCC
                                                                                                                                                                                                                                                                                                      AACACGCTAAATTTCAACGGAGCGCATCGTAAGAGGAAGACGCTGGTGGCCCCAGAGATC
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Location/Qualifiers
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BG912726
BG912726.1 GI:14293202
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

E. (bases 1 to 714)

S Birkett, C., Cho, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M., Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M., Zhang, X., Jay, G. and He, W.

High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts

Unpublished (2005)

Contact: Kovace, KF

High Throughput cDNA Cloning

Oricene Technologies, Inc. (www.origene.com)

6 Taft Court, Suite 100, Rockville, MD 20850, USA

Tel: 301 340 8606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR002011 714 bp mRNA linear EST 17-MAY-2005 TC120419 Human fetal brain, large insert, pCMV expression library Home sapiens cDNA clone TC120419 5' similar to Home sapiens DR12A1872 protein (KIAA1872), mRNA sequence.

DR002011 GI:66261884
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                                                                                                                                                                   301 CCCGATGAGACCGACTCGCTGGTGCTTCCTGGGGAATGGCAACGAACTGGAGTGGGAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 GAGCAAGAGCACCGTATAGACCTGCACATGATCCGGCCTTACATGAAAGTGGTCACCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601 GACAGCCTCNCCGACTACCACTACATCATGGAGAACCTCTTCCTGTACGTCATCAGC
                                            241 TCCGATGACTTCTTGGATACCCCTGATGACCTGGATATTAACGTGGATGACATCGAGACC
                                                                                                                                                                                                                                                      GACACCCCCTGGCCACCCACAAGAACATGCCCGGGGACAGCGCGGGATCTATTTGGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGCAAGAGCACCGTATAGACCTGCACATGATCCGGCCTTACATGAAAGTGGTCACCCAC
                                                                                                                               CCCGATGAGACCGACTCGCTGGAGTTCCTGGGGAATGGCAACGAACTGGAGTGGGAAGAC
                                                                                                                                                                                                                                                                                                                                                                            GGCACGACGACGCCAGCGCCCCAACGGGCGCCTGTGGCGGACAGTGATCATCGG
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This BST submission is part of an on-going human full-length
cloning project at OriGene Technologies, Inc.
Please contect OriGene for access.
OriGene Technologies, Inc.
6 Taft Ct. Suite 100
Rockville, MD 20850
Rockville, MJ 340-2188
http://www.origene.com
Seq primer: DCNV6 Sprime forward vector primer, OriGene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .714
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Technologies Inc.
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: Contact State Contact Conta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Pull-Length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Marc Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
results from a PCR reaction using an MGC full-length cDNA as
template DNA and ORF specific primers
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492
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                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/tiseuc_type="mixed"
/clone_lib="Full Length cDNA from the Mammalian Gene
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      sequence.
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Seg primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
      mRNA
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Insert Length: 699 Std Error: 65.00
BC026217,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence start: 98 High quality sequence stop: 698
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sapiens cDNA 5' similar to
                                                            CV024962.1 GI:51482851
                                                                                                                      Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                               Hominidae; Homo.
1 (bases 1 to 699)
                               CV024962
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TGACACCCAGCTCCTTTGAGAGGATCAGAGCCCATTGCACAAGAAGAGCCGCTGCCAACC 2146
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                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Hono.

1 (bases 1 to 876)

11 (bases 1 to 876)

Nath-MC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn67"
/note="Grgan: bfain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sali; Cloned unidirectionally, Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov
Plate: LLAM10866 row: k column: 18

High quality sequence stop: 693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:4941369"
/tissue_type="anaplastic oligodendroglioma with lp/19q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1788 CCCGCGTGGCGTCGGTGGCCTCCGCTCCTGCTCGCAGCCCCTGTGGTCAGAGCTGGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1848 AAGATTCAAGACCCTTCTCTTGCTTGTCACCCGCTCCAGGTTGGAGCCACAGACACCCAC
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22.4%; Score 653; DB 2;
Best Local Similarity 94.5%; Pred. No. 8.3e-90;
Matches 774; Conservative 0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                         GI:14294000
                                                                          Homo sapiens (human)
     mRNA sequence.
                                                                                               Homo sapiens
                                        BG913524.1
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           /mol_type="mRNA"
/do_xref="txxon:9606"
/clone="Tcl20419"
/tisuue type="Fetal Brain"
/clone_Tib="Human fetal brain, large insert, pCMV
expression library"
/note="Organ: Fetal Brain; Vector: pCMV6-XL4; Site 1:
RcoR1; Site_2: Xhol/Sall compatible end ligatio; Oligo-dr
primed reverse transcription optimized for large and GC
rich mRNA transcripts, cDNA size selection, optimized
ligation for large inserts into mammalian expression
vector, random clones selected for end sequence
verification of full-length genes"
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602811270F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4943369
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                                                                                                                                                                                                                                                                                          23.8%; Score 693.4; DB 8; Length 714; 99.9%; Pred. No. 6.1e-96; ive 0; Mismatches 1; Indels 0;
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'organism="Homo sapiens"
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Hominidae; Homo.

I (bases 1 to 639)

S Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES call growth and differentiation

L Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
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17000600176974 GRN_PRENEU Homo sapiens CDNA 5', mRNA seguence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                  421 TATGEGGACCTCACTGCTCCCCCAACCCAGGGTCAGGGTGGGGACATGCCAACGCTGTTCC
                                                                                              1906 ACCGCCACCCCGGCTGGGTCTGCGTCTTTCCTGTGCCTTTCCCTCCAGAATGCGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.26 GGGTTGGAACAGCAGAGGCTCAGAAACTGGCTCTGAAATAGGCAGACCTAGCAAGAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 GGGTTGGAACAGCAGGCTCAGAAACTGGCTCTGAAATAGGCAGACCTAGCAAGAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2386 GATACAGGGTATCGGGCGTTTGAGTGTTTCAGAAGTCATTCGGGAAGATAAATCCAGTGC
                                                       1 ACAAGATTCAAGACCCTTCTTTGCTTGTCACCCGCTCCAGGTTGGAGCCACAGACACCC
                                                                                                                        1966 AGACCTAGAAGCTCAACCCCCTATGAGGGCCACGTCCTGGGGTAGCTCCTGACCTCCGA
                                                                                                                                                                                          121 AGACCTAGAAGCTCAACCCCCCTATGAGGCCCACGTCCTGGGGTAGCTCCTGACCTCCGA
                                                                                                                                                                                                                         CCTTATGTCCAAATTTCACACCCATGGTTTTCATTTGACCCGCCCCCTTCTCGCTCATA
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                                  1846 ACAAGATTCAAGACCCTTCTCTTGCTTGTCACCCGCTCCAGGTTGGAGCCACAGACACCC
                                                                                                                                                                                                                                                                                     2086 ATGACACCCAGCTCCTTTGAGAGGATCAGAGCCCATTGCACAAGAAGAAGCCGCTGCCAAC
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DKFZp547E187 r1 547 (synonym: hfbr1) Homo sapiens cDNA clone
AL138250
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 650)

1 (bases 1 to 650)

EST (Ansorge, W., Wirkner, U., Mewes, W., Well, B. and Wiemann, S.
EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)
Unpublished (1999)
                                                               ATGTGGACCTCACTGCTCCCCCAACCCAGGGTCAGGCTGGGACACGCCAACGCTGTACCG
                                                                                                                             GGTTGGAACCAGCAGAGGCTCAGAAACTGGCCTCTGACATAGGCAGACCTAGCACGAGGA
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                                                                                                                                                                                                                                                                                                                      2385 AGATACAGGGTATCGGGCGTTTGAGTGTTTCAGAAGTCA-TTCGGGAAGATAAATCCAGT
                                               ATGTGGACCTCACTCCCCCCAACCCAGCGTCAGGCTGGGACACGCCAACGCTGTTCCG
                                                                                                           GGTTGGAA-CAGCAGAGGCTCAGAAACTGG-CTCTGAAATAGGCAGACCTAGCAAGAGGA
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/tissue_type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7" /clone lib="GRN PRENEU" /note="oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
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Bmail: rbrandenberger@geron.com
Insert Length: 639 Std Brror: 0.00.
Location/Qualifiers

    .639
    /organism="Homo sapiens"
/mol_type="mRNA"
    /db_xref="taxon:9606"

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